

```
=> file biosis caba caplus embase japio lifesci medline scisearch  
=> e kim bum joon/au
```

```
E1      50      KIM BUM JIN/AU  
E2      1      KIM BUM JO/AU  
E3    365 --> KIM BUM JOON/AU  
E4      3      KIM BUM JOON DR/AU  
E5      1      KIM BUM JOON DR PROF/AU  
E6     43      KIM BUM JUN/AU  
E7      1      KIM BUM JUNE/AU  
E8      1      KIM BUM KEE/AU  
E9      1      KIM BUM KEUM/AU  
E10     8      KIM BUM KEUN/AU  
E11     5      KIM BUM KI/AU  
E12     1      KIM BUM KOO/AU
```

```
=> s e1-e7 and mycobact? and HSP?
```

```
L2      48 ("KIM BUM JIN"/AU OR "KIM BUM JO"/AU OR "KIM BUM JOON"/AU OR  
        "KIM BUM JOON DR"/AU OR "KIM BUM JOON DR PROF"/AU OR "KIM BUM  
        JUN"/AU OR "KIM BUM JUNE"/AU) AND MYCOBACT? AND HSP?
```

```
=> dup rem 12
```

```
PROCESSING COMPLETED FOR L2
```

```
L3      14 DUP REM L2 (34 DUPLICATES REMOVED)
```

```
=> d bib ab kwic 1-
```

```
YOU HAVE REQUESTED DATA FROM 14 ANSWERS - CONTINUE? Y/(N):y
```

```
L3      ANSWER 1 OF 14 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 1  
AN      2008:1298911 CAPLUS <<LOGINID::20090924>>  
DN      151:27682  
TI      Proportions of ***Mycobacterium*** massiliense and  
        ***Mycobacterium*** bolletii strains among Korean ***Mycobacterium***  
        chelonae- ***Mycobacterium*** abscessus group isolates  
AU      Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam  
        Yong; Shim, Tae Sun; ***Kim, Bum-Joon*** ; Kook, Yoon-Hoh  
CS      Department of Microbiology, Cancer Research Institute, Institute of  
        Endemic Diseases, SNUMRC, and Clinical Research Institute, Seoul National  
        University College of Medicine, Seoul National University Hospital, Seoul,  
        110-799, S. Korea  
SO      Journal of Clinical Microbiology (2008), 46(10), 3384-3390  
CODEN: JCMIDW; ISSN: 0095-1137  
PB      American Society for Microbiology  
DT      Journal  
LA      English  
AB      Korean isolates of the ***Mycobacterium*** chelonae-  
        ***Mycobacterium*** abscessus group, which had been isolated from two  
        different hospitals in South Korea, were identified by PCR restriction  
        anal. (PRA) and comparative sequence anal. of 16S rRNA genes, rpoB, and  
        ***hsp65*** to evaluate the proportion of four closely related species  
        (M. chelonae, M. abscessus, M. massiliense, and M. bolletii). Of the 144  
        rapidly growing ***mycobacterial*** strains tested, 127 strains  
        (88.2%) belonged to the M. chelonae-M. abscessus group. In this group, M.  
        chelonae, M. abscessus, M. massiliense, and M. bolletii accounted for 0.8%  
        (n = 1), 51.2% (n = 65), 46.5% (n = 59), and 1.6% (n = 2), resp. Two  
        isolates which showed discordant results, M. massiliense by rpoB sequence  
        anal. and M. abscessus by ***hsp65*** sequence anal., were finally  
        identified as M. massiliense based on the addnl. anal. of sodA and the
```

16S-23S internal transcribed spacer. *M. abscessus* group I isolates previously identified by ***hsp65*** PRA were all found to be *M. abscessus*, whereas group II isolates were further identified as *M. massiliense* or *M. bolletii* by sequencing of rpoB and ***hsp65*** . Smooth, rough, or mixed colonies of both *M. abscessus* and *M. massiliense* isolates were obsd. *M. massiliense* strains that were highly resistant to clarithromycin had a point mutation at the adenine at position 2058 (A2058) or 2059 (A2059) in the peptidyltransferase region of the 23S rRNA gene.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Proportions of ***Mycobacterium*** massiliense and ***Mycobacterium*** bolletii strains among Korean ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group isolates

AU Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam Yong; Shim, Tae Sun; ***Kim, Bum-Joon*** ; Kook, Yoon-Hoh

AB Korean isolates of the ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group, which had been isolated from two different hospitals in South Korea, were identified by PCR restriction anal. (PRA) and comparative sequence anal. of 16S rRNA genes, rpoB, and ***hsp65*** to evaluate the proportion of four closely related species (*M. chelonae*, *M. abscessus*, *M. massiliense*, and *M. bolletii*). Of the 144 rapidly growing ***mycobacterial*** strains tested, 127 strains (88.2%) belonged to the *M. chelonae*-*M. abscessus* group. In this group, *M. chelonae*, *M. abscessus*, M... . . (n = 2), resp. Two isolates which showed discordant results, *M. massiliense* by rpoB sequence anal. and *M. abscessus* by ***hsp65*** sequence anal., were finally identified as *M. massiliense* based on the addnl. anal. of sodA and the 16S-23S internal transcribed spacer. *M. abscessus* group I isolates previously identified by ***hsp65*** PRA were all found to be *M. abscessus*, whereas group II isolates were further identified as *M. massiliense* or *M. bolletii* by sequencing of rpoB and ***hsp65*** . Smooth, rough, or mixed colonies of both *M. abscessus* and *M. massiliense* isolates were obsd. *M. massiliense* strains that were. . .

ST ***Mycobacterium*** antibiotic resistance clarithormycin taxonomy
IT rRNA

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(23 S; proportions of ***Mycobacterium*** massiliense and ***Mycobacterium*** bolletii strains among Korean ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group isolates)

IT Mutation
(point; proportions of ***Mycobacterium*** massiliense and ***Mycobacterium*** bolletii strains among Korean ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group isolates)

IT Antibiotic resistance
Mycobacterium abscessus
Mycobacterium bolletii
Mycobacterium chelonae
Mycobacterium massiliense
(proportions of ***Mycobacterium*** massiliense and ***Mycobacterium*** bolletii strains among Korean ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group isolates)

IT 81103-11-9, Clarithromycin

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proportions of ***Mycobacterium*** massiliense and
Mycobacterium bolletii strains among Korean
Mycobacterium chelonae- ***Mycobacterium*** abscessus group
isolates)

L3 ANSWER 2 OF 14 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 2

AN 2008:322988 BIOSIS <>LOGINID::20090924>>

DN PREV200800322987

TI ***Mycobacterium*** senuense sp nov., a slowly growing,
non-chromogenic species closely related to the ***Mycobacterium***
terrae complex.

AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil;
Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol and Immunol, Canc Res Inst,
Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (MAR
2008) Vol. 58, No. Part 3, pp. 641-646.
ISSN: 1466-5026.

DT Article

LA English

OS GenBank-DQ536407; EMBL-DQ536407; DDJB-DQ536407; GenBank-DQ536409;
EMBL-DQ536409; DDJB-DQ536409

ED Entered STN: 29 May 2008
Last Updated on STN: 29 May 2008

AB A previously undescribed, slowly growing, non-chromogenic
mycobacterium, isolated from a Korean patient with a symptomatic
pulmonary infection, is described as representing a novel species. Its
16S rRNA gene sequence was unique and phylogenetic analysis based on 16S
rRNA gene sequences showed that this organism belonged to the
Mycobacterium terrae subclade. Phenotypically, the strain was
generally similar to M. terrae and ***Mycobacterium***
nonchromogenicum, but its growth rate was slower than those of other M.
terrae complex strains. A unique mycolic acid profile and phylogenetic
analysis based on two different alternative chronometer molecules,
hsp65 and rpoB, confirm the taxonomic status of this strain as a
representative of a novel species. The name ***Mycobacterium***
senuense sp. nov. is proposed, with the type strain 05-832(T) (=DSM
44999(T) =KCTC 19147(T)).

TI ***Mycobacterium*** senuense sp nov., a slowly growing,
non-chromogenic species closely related to the ***Mycobacterium***
terrae complex.

AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil;
Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]

AB A previously undescribed, slowly growing, non-chromogenic
mycobacterium, isolated from a Korean patient with a symptomatic
pulmonary infection, is described as representing a novel species. Its
16S rRNA. . . gene sequence was unique and phylogenetic analysis based
on 16S rRNA gene sequences showed that this organism belonged to the
Mycobacterium terrae subclade. Phenotypically, the strain was
generally similar to M. terrae and ***Mycobacterium***
nonchromogenicum, but its growth rate was slower than those of other M.
terrae complex strains. A unique mycolic acid profile and phylogenetic
analysis based on two different alternative chronometer molecules,
hsp65 and rpoB, confirm the taxonomic status of this strain as a

representative of a novel species. The name ***Mycobacterium*** senuense sp. nov. is proposed, with the type strain 05-832(T) (=DSM 44999(T) =KCTC 19147(T)).

IT Major Concepts
Population Genetics (Population Studies); Systematics and Taxonomy

IT Chemicals & Biochemicals
rpoB; ***hsp65*** ; 16S ribosomal RNA [16S rRNA, gene sequence]

ORGN . . .
Chordata; Animalia

Organism Name
human (common): aged, host, Korean, male

Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Mycobacteriaceae *08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium terrae (species)
Mycobacterium nonchromogenicum (species)
Mycobacterium senuense (species): new species, description,
strain-05-832-T

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L3 ANSWER 3 OF 14 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 3

AN 2008:636733 BIOSIS <>LOGINID::20090924>>

DN PREV200800636732

TI Differentiation of ***mycobacteria*** in sputa by duplex polymerase chain reaction for ***mycobacterial*** ***hsp65*** gene.

AU ***Kim, Bum-Joon*** [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Eui-Chong; Joo, Sei Ick; Lee, Jae Seok; Yim, Jae-Joon

CS Seoul Natl Univ, Coll Med, Canc Res Inst, Dept Microbiol and Immunol, Seoul 110744, South Korea
kbumjoon@snu.ac.kr; yimjj@snu.ac.kr

SO Diagnostic Microbiology and Infectious Disease, (OCT 2008) Vol. 62, No. 2, pp. 193-198.
CODEN: DMIDDZ. ISSN: 0732-8893.

DT Article

LA English

ED Entered STN: 19 Nov 2008
Last Updated on STN: 19 Nov 2008

AB Early differentiation of ***mycobacteria*** in Sputa is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating ***mycobacteria*** in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. ***Mycobacterial*** species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of ***mycobacterial*** species were made based on 1) results of species identification based on ***mycobacterial*** colonies or 2) results of species identification of other sputa from the same patients and clinical findings. The duplex

PCR-based method correctly identified 83.2% Sputa from tuberculosis patients and 82.2% sputa from nontuberculous ***mycobacteria*** patients, whereas the colonybased method correctly identified 86.1% and 77.8%, respectively. Sensitivity and specificity of the colony-based method for ***Mycobacterium*** tuberculosis were 86.1% and 100%, respectively, whereas those of the duplex PCR-based method were 83.2% and 95.6%, respectively. The duplex PCR-based method, to differentiate ***mycobacterial*** species in Sputa, produced comparable results as those of the colony-based identification method. (C) 2008 Elsevier Inc. All rights reserved.

TI Differentiation of ***mycobacteria*** in sputa by duplex polymerase chain reaction for ***mycobacterial*** ***hsp65*** gene.

AU ***Kim, Bum-Joon*** [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Eui-Chong; Joo, Sei Ick; Lee, Jae. . .

AB Early differentiation of ***mycobacteria*** in Sputa is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating ***mycobacteria*** in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. ***Mycobacterial*** species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of ***mycobacterial*** species were made based on 1) results of species identification based on ***mycobacterial*** colonies or 2) results of species identification of other sputa from the same patients and clinical findings. The duplex PCR-based method correctly identified 83.2% Sputa from tuberculosis patients and 82.2% sputa from nontuberculous ***mycobacteria*** patients, whereas the colonybased method correctly identified 86.1% and 77.8%, respectively. Sensitivity and specificity of the colony-based method for ***Mycobacterium*** tuberculosis were 86.1% and 100%, respectively, whereas those of the duplex PCR-based method were 83.2% and 95.6%, respectively. The duplex PCR-based method, to differentiate ***mycobacterial*** species in Sputa, produced comparable results as those of the colony-based identification method. (C) 2008 Elsevier Inc. All rights reserved.

IT Major Concepts

Methods and Techniques; Infection; Molecular Genetics (Biochemistry and Molecular Biophysics); Human Medicine (Medical Sciences)

IT Diseases

Mycobacterium infection: bacterial disease, diagnosis

ORGN . . .

Primates; Mammalia; Vertebrata; Chordata; Animalia

Organism Name

human (common): host

Taxa Notes

Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier

Mycobacteriaceae 08881

Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms;

Eubacteria; Bacteria; Microorganisms

Organism Name

Mycobacterium tuberculosis (species): pathogen

Mycobacterium abscessus (species): pathogen

Mycobacterium avium (species): pathogen

Mycobacterium intracellularare (species): pathogen
 Mycobacterium fortuitum (species): pathogen
 Mycobacterium chelonae (species): pathogen
 Mycobacterium kansasii (species): pathogen
 Mycobacterium parascrofulaceum (species): pathogen

Taxa Notes

Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** ***hsp65*** gene (***Mycobacteriaceae***)

L3 ANSWER 4 OF 14 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2007:1057364 CAPLUS <>LOGINID::20090924>>

DN 147:337125

TI Method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence

IN ***Kim, Bum Joon*** ; Kim, Hyun Joo; Park, Hae Joon

PA Seoul National University Industry Foundation, S. Korea

SO Repub. Korea, No pp. given

CODEN: KRXXFC

DT Patent

LA Korean

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 692484	B1	20070313	KR 2005-104871	20051103
PRAI	KR 2005-104871		20051103		
AB	A method for identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** is provided to conveniently and accurately differentiate ***Mycobacterial*** species by using each 8 signature nucleotide sequences capable of characterizing ***Mycobacterium*** tuberculosis group and non-tuberculous ***mycobacteria*** group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the group consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of ***Mycobacterial*** species using a primer specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the bases above to identify non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis, where the non-tuberculous ***mycobacteria*** is 228th base of C, 243th base of C, 543th base of C,				
C,	600th base of C or T, 705th base of G or 718-720th bases of CAG, and the ***Mycobacterium*** tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base of C or 718-720th bases of GGA. The nucleotide sequence of primer pair for producing PCR amplification product specific to the non-tuberculous ***mycobacteria*** is described. The differentiation kit for non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis comprises a primer pairs, and the sequences of the primers have been presented.				

TI Method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence

IN ***Kim, Bum Joon*** ; Kim, Hyun Joo; Park, Hae Joon

AB A method for identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** is provided to conveniently and accurately differentiate ***Mycobacterial*** species by using each 8

signature nucleotide sequences capable of characterizing ***Mycobacterium*** tuberculosis group and non-tuberculous ***mycobacteria*** group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the . . . consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of ***Mycobacterial*** species using a primer specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the bases above to identify non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis, where the non-tuberculous ***mycobacteria*** is 228th base of C, 243th base of C, 543th base of C, 600th base of C or T, 705th base of G or 718-720th bases of CAG, and the ***Mycobacterium*** tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base. . . or 718-720th bases of GGA. The nucleotide sequence of primer pair for producing PCR amplification product specific to the non-tuberculous ***mycobacteria*** is described. The differentiation kit for non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis comprises a primer pairs, and the sequences of the primers have been presented.

ST ***Mycobacterium*** tuberculosis nontuberculous genotyping PCR
Hsp65 gene

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** 65; method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***hsp65*** ; method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence)

IT Genotypes
Genotyping (method)
Mycobacterium
Mycobacterium tuberculosis

Polymerase chain reaction
Tuberculosis
(method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence)

L3 ANSWER 5 OF 14 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:1225201 SCISEARCH <<LOGINID::20090924>>
GA The Genuine Article (R) Number: 231FU
TI Case of pyomyositis due to ***Mycobacterium*** haemophilum in a renal transplant recipient

AU Choi, Sang-Ho (Reprint)
CS Univ Ulsan, Coll Med, Asan Med Ctr, Div Infect Dis, Seoul 138736, South Korea (Reprint)
AU Jang, Eun-Young; Lee, Sang-Oh; Choi, Seong-Ho; Sung, Heungsup; Kim, Mi-Na;
Kim, Bum-Joon ; Kim, Yang Soo; Woo, Jun Hee
CS Univ Ulsan, Coll Med, Asan Med Ctr, Dept Lab Med, Seoul 138736, South Korea; Seoul Natl Univ, Coll Med, Liver Res Inst, Canc Res Inst, Dept Microbiol & Immunol, Seoul, South Korea
E-mail: sangho@amc.seoul.kr
CYA South Korea
SO JOURNAL OF CLINICAL MICROBIOLOGY, (NOV 2007) Vol. 45, No. 11, pp.
3847-3849.
ISSN: 0095-1137.
PB AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
DT Article; Journal
LA English
REC Reference Count: 13
ED Entered STN: 13 Dec 2007
Last Updated on STN: 13 Dec 2007
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB We report a case of pyomyositis due to ***Mycobacterium*** haemophilum in a renal transplant recipient. *M. haemophilum* was identified by PCR-mediated sequence analysis of the heat shock protein gene in the DNA of the specimen. The patient was successfully treated with repeated surgical debridement and prolonged anti-***mycobacterial*** therapy.
TI Case of pyomyositis due to ***Mycobacterium*** haemophilum in a renal transplant recipient
AU Jang, Eun-Young; Lee, Sang-Oh; Choi, Seong-Ho; Sung, Heungsup; Kim, Mi-Na;
Kim, Bum-Joon ; Kim, Yang Soo; Woo, Jun Hee
AB We report a case of pyomyositis due to ***Mycobacterium*** haemophilum in a renal transplant recipient. *M. haemophilum* was identified by PCR-mediated sequence analysis of the heat shock protein gene in the DNA of the specimen. The patient was successfully treated with repeated surgical debridement and prolonged anti-***mycobacterial*** therapy.
STP KeyWords Plus (R): GENE ***HSP65*** ; IDENTIFICATION; PATIENT; RPOB;
AVIUM; AIDS

L3 ANSWER 6 OF 14 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 4
AN 2007:1135732 CAPLUS <<LOGINID::20090924>>
DN 148:281748
TI Outbreak of ***Mycobacterium*** massiliense infection associated with intramuscular injections
AU Kim, Hee-Youn; Yun, Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo;
Kim, Bum-Joon ; Kook, Yoon-Hoh
CS Department of Microbiology, Cancer Research Institute, Institute of Endemic Diseases, SNUMRC, S. Korea
SO Journal of Clinical Microbiology (2007), 45(9), 3127-3130
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Twelve strains of a rapidly growing ***Mycobacterium*** species were isolated from an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and

hsp65 . These isolates were identified as ***Mycobacterium*** massiliense (100% similarity).

OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Outbreak of ***Mycobacterium*** massiliense infection associated with intramuscular injections

AU . . . Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; ***Kim,*** Bum-Joon*** ; Kook, Yoon-Hoh

AB Twelve strains of a rapidly growing ***Mycobacterium*** species were isolated from an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65*** . These isolates were identified as ***Mycobacterium*** massiliense (100% similarity).

ST ***Mycobacterium*** infection ribostamycin intramuscular injection antibiotic susceptibility; gene sequence rpoB ***hsp65*** ***Mycobacterium*** infection taxonomy epidemiol

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(***HSP*** 65, gene ***hsp65*** ; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)

IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(***hsp65*** ; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)

IT Bacterial infection

(i.m. injection-assocd. infection; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)

IT Pharmaceutical injections

(i.m. injections, i.m. injection-assocd. infection; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)

IT Evolution

(mol., rpoB and ***hsp65*** sequence phylogeny; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)

IT Epidemiology

Taxonomy

(mol.; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)

IT Antibiotic resistance

DNA sequences

Mycobacterium abscessus
Mycobacterium aichiense
Mycobacterium hassiacum
Mycobacterium massiliense
Mycobacterium parafortuitum

Protein sequences

(outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)

IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(rpoB; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)
IT 564-25-0, Doxycycline 10118-90-8, Minocycline 37517-28-5, Amikacin 81103-11-9, Clarithromycin 83905-01-5, Azithromycin
RL: BSU (Biological study, unclassified); PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(***Mycobacterium*** susceptibility; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)
IT 1007444-81-6 1007444-83-8 1007444-85-0 1007444-87-2 1007444-89-4
1008181-63-2 1008181-65-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)
IT 53797-35-6, Ribostamycin sulfate
RL: ADV (Adverse effect, including toxicity); PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(i.m. injection-assocd. infection; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)
IT 1007444-80-5 1007444-82-7 1007444-84-9 1007444-86-1 1007444-88-3
1008181-62-1 1008181-64-3
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)
IT 9014-24-8, RNA polymerase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(.beta. subunit, gene rpoB; outbreak of ***Mycobacterium*** massiliense infection assocd. with i.m. injections)

L3 ANSWER 7 OF 14 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:1211730 SCISEARCH <<LOGINID::20090924>>
GA The Genuine Article (R) Number: 228MD
TI Pulmonary disease caused by ***Mycobacterium*** xenopi: The first case in Korea
AU Koh, Won-Jung (Reprint)
CS Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Med, Div Pulm & Crit Care Med, 50 Irwan Dong, Seoul, South Korea (Reprint)
AU Park, Hye Yun; Kwon, O. Jung; Lee, Nam Yong; Shim, Young Mog; Park, Young Kil; Bai, Gill Han; Mun, Ho-Suk; ***Kim, Bum-Joon***
CS Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Med, Div Pulm & Crit Care Med, Seoul, South Korea; Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Lab Med, Seoul, South Korea; Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Thorac Surg, Seoul, South Korea; Korean Natl TB Assoc, Korean Inst TB, Seoul, South Korea; Seoul Natl Univ, Coll Med, Dept Microbiol & Immunol, Seoul, South Korea; Seoul Natl Univ, Coll Med, Canc Res Inst, Seoul, South Korea
E-mail: wjkoh@skku.edu
CYA South Korea
SO YONSEI MEDICAL JOURNAL, (31 OCT 2007) Vol. 48, No. 5, pp. 871-875.
ISSN: 0513-5796.
PB YONSEI UNIV COLLEGE MEDICINE, C/O KYUN0-IL IM, M.D., PH.D, SHINCHON DONG 134, SEODAEMOON KU, SEOUL 120-752, SOUTH KOREA.
DT Article; Journal

LA English
REC Reference Count: 20
ED Entered STN: 6 Dec 2007
Last Updated on STN: 6 Dec 2007
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB ***Mycobacterium*** xenopi is a nontuberculous
 mycobacterium (NTM) that rarely causes pulmonary disease in Asia.
Here we describe the first case of M xenopi pulmonary disease in Korea. A 66-year-old man was admitted to our hospital with a 2-month history of productive cough and hemoptysis. His past medical history included pulmonary tuberculosis 44 years earlier, leading to a right upper lobectomy. Chest X-ray upon admission revealed cavitary consolidation involving the entire right lung. Numerous acid-fast bacilli were seen in his initial sputum, and M xenopi was subsequently identified in more than five sputum cultures, using molecular methods. Despite treatment with clarithromycin, rifampicin, ethambutol, and streptomycin, the infiltrative shadow revealed on chest X-ray increased in size. The patient's condition worsened, and a right completion pneumonectomy was performed. The patient consequently died of respiratory failure on postoperative day 47, secondary to the development of a late bronchopleural fistula. This case serves as a reminder to clinicians that the incidence of NTM infection is increasing in Korea and that unusual NTM are capable of causing disease in non-immunocompromised patients.

TI Pulmonary disease caused by ***Mycobacterium*** xenopi: The first case in Korea
AU . . Park, Hye Yun; Kwon, O. Jung; Lee, Nam Yong; Shim, Young Mog; Park, Young Kil; Bai, Gill Han; Mun, Ho-Suk; ***Kim, Bum-Joon***
AB ***Mycobacterium*** xenopi is a nontuberculous
 mycobacterium (NTM) that rarely causes pulmonary disease in Asia.
Here we describe the first case of M xenopi pulmonary disease in . . .
ST Author Keywords: atypical ***mycobacteria*** ; ***Mycobacterium***
xenopi; Korea
STP KeyWords Plus (R): NONTUBERCULOUS ***MYCOBACTERIA*** ; INFECTIO; DIFFERENTIATION; CLARITHROMYCIN; SPECIMENS; PATIENT; ***HSP65*** ; GENE

L3 ANSWER 8 OF 14 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 5
AN 2007:338789 BIOSIS <>LOGINID::20090924>>
DN PREV200700342042
TI ***Mycobacterium*** seoulense sp nov., a slowly growing
 scotochromogenic species.
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, ***
 *** Bum-Joon*** [Reprint Author]
CS Seoul Natl Univ, Dept Microbiol and Immunol, Canc Res Inst, Coll Med,
Seoul 110799, South Korea
kbumjoon@snu.ac.kr
SO International Journal of Systematic and Evolutionary Microbiology, (MAR
2007) Vol. 57, No. Part 3, pp. 594-599.
ISSN: 1466-5026.
DT Article
LA English
ED Entered STN: 6 Jun 2007
Last Updated on STN: 6 Jun 2007
AB A. previously undescribed, slowly growing, scotochromogenic
 mycobacterium was isolated from a patient with symptomatic
pulmonary infection during ***hsp65*** sequence-based identification

of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of ***Mycobacterium*** nebraskense and ***Mycobacterium*** scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic analysis based on 16S rRNA gene sequences placed the organism in the slowly growing ***Mycobacterium*** group close to *M. nebraskense* and *M. scrofulaceum*. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and *rpoB*, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel ***mycobacterial*** species, for which the name ***Mycobacterium*** seoulense sp. nov. is proposed. The type strain is strain 03-19(T) (=DSM 44998(T)=KCTC 19146(T)).

TI ***Mycobacterium*** seoulense sp nov., a slowly growing scotochromogenic species.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** *** Bum-Joon*** [Reprint Author]

AB A. previously undescribed, slowly growing, scotochromogenic ***mycobacterium*** was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of ***Mycobacterium*** nebraskense and ***Mycobacterium*** scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic analysis based on 16S rRNA gene sequences placed the organism in the slowly growing

Mycobacterium group close to *M. nebraskense* and *M. scrofulaceum*. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and *rpoB*, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel ***mycobacterial*** species, for which the name ***Mycobacterium*** seoulense sp. nov. is proposed. The type strain is strain 03-19(T) (=DSM 44998(T)=KCTC 19146(T)).

IT . . .
Medicine (Human Medicine, Medical Sciences); Systematics and Taxonomy
IT Parts, Structures, & Systems of Organisms
lung: respiratory system

IT Diseases
Mycobacterium infection: bacterial disease, infectious disease, genetics

IT Diseases
pulmonary infection: respiratory system disease, infectious disease, bacterial disease, symptom, genetics
Respiratory Tract. . .

ORGN . . .
Animalia
Organism Name
human (common): middle age, host, Korean, female

Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Mycobacteriaceae *08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;

Eubacteria; Bacteria; Microorganisms
 Organism Name

ATCC	***Mycobacterium***	leprae (species): pathogen
	Mycobacterium	tuberculosis (species): pathogen
	Mycobacterium	marinum (species): pathogen
	Mycobacterium	haemophilum (species): pathogen
	Mycobacterium	ulcerans (species): pathogen
	Mycobacterium	intracellulare (species): pathogen, strain-
13950	***Mycobacterium***	seoulense (species): new species, pathogen,
	description, rod-shaped, strain-KCTC 19146	bent cell, strain-03-19, strain-DSM 44998,
	Mycobacterium	nebraskense (species): pathogen, strain-YNMC-
MY	1349	scrofulaceum (species): pathogen, strain-DSM
	Mycobacterium	avium (species): pathogen, strain-DSM 44156
	43992	(genus): pathogen, strain-IWGMT 90160
	Mycobacterium	gastri (species): pathogen, strain-ATCC 15754
	Mycobacterium	kansasii (species): pathogen, strain-ATCC
12478	***Mycobacterium***	paratuberculosis (species): pathogen,
	strain-ATCC 19698	malmoense (species): pathogen, strain-ATCC
	Mycobacterium	szulgai (species): pathogen, strain-ATCC 35799
	29571	simiae (species): pathogen, strain-ATCC 25275

Taxa Notes
 Bacteria, Eubacteria, Microorganisms

ORGN Classifier
 Nocardioform Actinomycetes 08810

Super Taxa
 Actinomycetes and Related. . .

GEN ***Mycobacterium*** ***hsp65*** gene [***Mycobacterium*** heat shock protein 65 gene] (***Mycobacteriaceae***): expression;

Mycobacterium rpoB gene (***Mycobacteriaceae***): expression

L3 ANSWER 9 OF 14 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2007:465634 CAPLUS <>LOGINID::20090924>>
 DN 147:339410
 TI ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species
 AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** Bum-Joon***
 CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea
 SO International Journal of Systematic and Evolutionary Microbiology (2007), 57(3), 593-599
 CODEN: ISEMF5; ISSN: 1466-5026
 PB Society for General Microbiology
 DT Journal
 LA English
 AB A previously undescribed, slowly growing, scotochromogenic

mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of ***Mycobacterium*** nebraskense and ***Mycobacterium*** scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic anal. based on 16S rRNA gene sequences placed the organism in the slowly growing ***Mycobacterium*** group close to M. nebraskense and M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel ***mycobacterial*** species, for which the name ***Mycobacterium*** seoulense sp. nov. is proposed. The type strain is strain 03-19T (= DSM 44998T = KCTC 19146T).

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

- TI ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species
- AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, *** Bum-Joon***
- AB A previously undescribed, slowly growing, scotochromogenic ***mycobacterium*** was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of ***Mycobacterium*** nebraskense and ***Mycobacterium*** scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic anal. based on 16S rRNA gene sequences placed the organism in the slowly growing ***Mycobacterium*** group close to M. nebraskense and M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel ***mycobacterial*** species, for which the name ***Mycobacterium*** seoulense sp. nov. is proposed. The type strain is strain 03-19T (= DSM 44998T = KCTC 19146T).
- ST ***Mycobacterium*** scotochromogenic 16S rRNA gene rpoB ***hsp65*** sequence
- IT rRNA
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(16 S; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)
- IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(16S rRNA; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)
- IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** 65; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT DNA sequences
Human
 Mycobacterium seoulense
Protein sequences
 (***Mycobacterium*** seoulense sp. nov., a slowly growing
 scotochromogenic species)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (***hsp65*** ; ***Mycobacterium*** seoulense sp. nov., a slowly
 growing scotochromogenic species)
IT Evolution
 (mol., phylogeny; ***Mycobacterium*** seoulense sp. nov., a slowly
 growing scotochromogenic species)
IT Taxonomy
 (mol.; ***Mycobacterium*** seoulense sp. nov., a slowly growing
 scotochromogenic species)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (rpoB; ***Mycobacterium*** seoulense sp. nov., a slowly growing
 scotochromogenic species)
IT 9014-24-8, RNA polymerase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (***Mycobacterium*** seoulense sp. nov., a slowly growing
 scotochromogenic species)
IT 948634-47-7 948634-50-2
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; ***Mycobacterium*** seoulense sp. nov., a
 slowly growing scotochromogenic species)
IT 948634-46-6 948634-48-8 948634-49-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide sequence; ***Mycobacterium*** seoulense sp. nov., a
 slowly growing scotochromogenic species)

L3 ANSWER 10 OF 14 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 6
AN 2007:135186 BIOSIS <>LOGINID::20090924>>
DN PREV200700134974
TI Direct application of AvaII PCR restriction fragment length polymorphism
analysis (AvaII PRA) targeting 644 bp heat shock protein 65 (***hsp65***
) gene to sputum samples.
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai,
 Gil-Han; Do, Junghwan; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon*** [Reprint Author]
CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799,
 South Korea
 kbumjoon@snu.ac.kr
SO Microbiology and Immunology, (2007) Vol. 51, No. 1, pp. 105-110.
 CODEN: MIIMDV. ISSN: 0385-5600.
DT Article
LA English
ED Entered STN: 22 Feb 2007
 Last Updated on STN: 22 Feb 2007

AB To evaluate the usefulness of the Avall PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic ***mycobacteria*** from clinical specimens, we applied this method to
40 sputum samples and compared the results to those obtained by IS6110 PCR. Although this method showed a sensitivity slightly lower than IS6110 PCR (97.5% vs. 100%), it detected infections of M. avium complex (MAC) in two patients, which was not possible by IS6110 PCR. We conclude that Avall PRA is a highly effective method for directly detecting pathogenic ***mycobacteria*** in primary clinical specimens.

TI Direct application of Avall PCR restriction fragment length polymorphism analysis (Avall PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai, Gil-Han; Do, Junghwan; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon*** [Reprint Author]

AB To evaluate the usefulness of the Avall PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic ***mycobacteria*** from clinical specimens, we applied this method to
40 sputum samples and compared the results to those obtained by IS6110. . . . was not possible by IS6110 PCR. We conclude that Avall PRA is a highly effective method for directly detecting pathogenic ***mycobacteria*** in primary clinical specimens.

IT . . .
Infection; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Parts, Structures, & Systems of Organisms
sputum

IT Diseases
Mycobacterium avium infection: bacterial disease, infectious disease

IT Diseases
Mycobacterium tuberculosis infection: bacterial disease, infectious disease

IT Chemicals & Biochemicals
644 bp

ORGN . . .
Primates; Mammalia; Vertebrata; Chordata; Animalia
Organism Name
human (common): host

Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium tuberculosis (species): pathogen
Mycobacterium avium (species): pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** avium ***hsp65*** gene [***Mycobacterium*** avium heat shock protein 65 gene] (***Mycobacteriaceae***): expression; ***Mycobacterium*** tuberculosis ***hsp65*** gene [***Mycobacterium*** tuberculosis heat shock protein 65 gene] (

Mycobacteriaceae): expression

L3 ANSWER 11 OF 14 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 7
AN 2006:1304935 CAPLUS <>LOGINID::20090924>>
DN 146:515458
TI Differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing
AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, *** Bum-Joon***
CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea
SO Journal of Clinical Microbiology (2006), 44(11), 3855-3862
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Here we describe a novel duplex PCR method which can differentiate ***Mycobacterium*** tuberculosis and nontuberculosis ***mycobacteria*** (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin. isolates and differentiated all strains into their resp. groups with 100% sensitivity and specificity. Furthermore, a duplex PCR-restriction anal. (duplex PRA) and a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and subspecies levels by subsequent procedures (PRA or direct sequencing) targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for identifying ***mycobacterial*** culture isolates at the species level.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing
AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, *** Bum-Joon***
AB Here we describe a novel duplex PCR method which can differentiate ***Mycobacterium*** tuberculosis and nontuberculosis ***mycobacteria*** (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin.. . . a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and. . . targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for identifying ***mycobacterial*** culture isolates at the species level.
ST ***Mycobacterium*** species differentiation ***hsp65*** duplex PCR restriction analysis sequencing

IT DNA sequence analysis
 Mycobacterium tuberculosis

Tuberculosis
 (differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Genetic methods
by
 (duplex-PCR-based restriction anal.; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Polymerase chain reaction
anal.
 (duplex; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
anal.
 (***hsp65*** ; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Human
anal.
 (isolates from; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Diagnosis
anal.
 (mol.; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT ***Mycobacterium***
anal.
 (nontuberculosis; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT 936858-56-9 936858-57-0 936858-58-1 936858-59-2 936858-60-5
936858-61-6 936858-62-7 936858-64-9 936858-65-0

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
anal.
 (primer; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

L3 ANSWER 12 OF 14 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 8

AN 2005:448449 BIOSIS <>LOGINID::20090924>>

DN PREV200510237956

TI Differentiation of ***Mycobacterium*** species by analysis of the heat-shock protein 65 gene (***hsp65***).

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (JUL 2005) Vol. 55, No. Part 4, pp. 1649-1656.
ISSN: 1466-5026.

DT Article

LA English

ED Entered STN: 3 Nov 2005
Last Updated on STN: 3 Nov 2005

AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 ***Mycobacterium*** strains containing 56 reference ***Mycobacterium*** species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between ***Mycobacterium*** species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene, thus revealing natural relationships among ***Mycobacterium*** species. When a direct sequencing protocol targeting 422 bp sequences was applied to 70 non-tuberculous ***mycobacterium*** (NTM) clinical isolates, all NTMs were clearly identified. In addition, an Xhol PCR restriction fragment length polymorphism analysis method for the differentiation of ***Mycobacterium*** , tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of ***mycobacteria*** .

TI Differentiation of ***Mycobacterium*** species by analysis of the heat-shock protein 65 gene (***hsp65***).

AU. . . Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]

AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 ***Mycobacterium*** strains containing 56 reference ***Mycobacterium*** species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between ***Mycobacterium*** species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene, thus revealing natural relationships among ***Mycobacterium*** species. When a direct sequencing protocol targeting 422 bp sequences was applied to 70 non-tuberculous ***mycobacterium*** (NTM) clinical isolates, all NTMs were clearly identified. In addition, an Xhol PCR restriction fragment length polymorphism analysis method for the differentiation of ***Mycobacterium*** , tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of ***mycobacteria*** .

IT . . .

Genetics (Population Studies); Systematics and Taxonomy

IT Chemicals & Biochemicals
16S rRNA [16S ribosomal RNA]; endonuclease; heat shock protein 65 [***HSP65***]

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium tuberculosis (species)
Mycobacterium (genus)

Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** 16S rRNA gene (***Mycobacteriaceae***);
Mycobacterium ***hsp65*** gene [***Mycobacterium***
heat-shock protein 65 gene gene] (***Mycobacteriaceae***)

L3 ANSWER 13 OF 14 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 9

AN 2005:437869 BIOSIS <>LOGINID::20090924>>

DN PREV200510224308

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of ***Mycobacterium*** spp.

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** *** Bum-Joon*** [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO Journal of Microbiological Methods, (AUG 2005) Vol. 62, No. 2, pp. 199-209.
CODEN: JMIMDQ. ISSN: 0167-7012.

DT Article

LA English

ED Entered STN: 26 Oct 2005
Last Updated on STN: 26 Oct 2005

AB A method based on PCR-restriction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of ***mycobacteria*** to the species level. A 644 bp region of ***hsp65*** in 62 ***mycobacteria*** reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, Avall, HphI, and HpaII. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the separation of M avium, M intracellulare and M tuberculosis to the species level by Avall digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clinical isolates, which had been characterized by conventional biochemical testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of ***mycobacteria*** culture isolates at the species level. (c) 2005 Elsevier B.V. All rights reserved.

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for

AU differentiation of ***Mycobacterium*** spp.
AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park,
AU Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
AU *** Bum-Joon*** [Reprint Author]
AB A method based on PCR-restriction fragment length polymorphism analysis
(PRA) using a novel region of the ***hsp65*** gene was developed for
the rapid and exact identification of ***mycobacteria*** to the
species level. A 644 bp region of ***hsp65*** in 62
mycobacteria reference strains, and 4 related bacterial strains
were amplified, and the amplified DNAs were subsequently digested with
restriction enzymes, namely, AvaII, HphI, and HpaII. Most of the
mycobacteria species were easily differentiated at the species
level by the developed method. In particular, the method enabled the
separation of. . . biochemical testing. Our results suggest that this
novel PRA offers a simple, rapid, and accurate method for the
identification of ***mycobacteria*** culture isolates at the species
level. (c) 2005 Elsevier B.V. All rights reserved.

ORGN . . .
Organisms 08800
Super Taxa
Eubacteria; Bacteria; Microorganisms
Organism Name
Tsukamurella paurometabola (species): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms
ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium tuberculosis (species): pathogen
Mycobacterium avium (species): pathogen
Mycobacterium intracellulare (species): pathogen
Mycobacterium (genus): pathogen, 62 species
Taxa Notes
Bacteria, Eubacteria, Microorganisms
ORGN Classifier
Nocardioform Actinomycetes 08810
Super Taxa
Actinomycetes and Related Organisms; . . .
GEN ***Mycobacterium*** ***hsp65*** gene [***Mycobacterium*** heat
shock protein 65 gene] (***Mycobacteriaceae***)

L3 ANSWER 14 OF 14 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:591378 CAPLUS <>LOGINID::20090924>>
DN 139:146183
TI Primers for amplifying ***mycobacterial*** heat shock protein
HSP 65 gene and use for identifying ***mycobacterial***
species
IN ***Kim, Bum-joon*** ; Kook, Yoon-ho; Kim, Jeong-mi
PA Biomedlab Corporation, S. Korea
SO PCT Int. Appl., 102 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305
	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB The present invention relates to a pair of primers specific to ***mycobacterial*** species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of ***mycobacterial*** species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the ***mycobacterial*** species can be identified simply, economically, and accurately.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species

IN ***Kim, Bum-joon*** ; Kook, Yoon-ho; Kim, Jeong-mi

AB The present invention relates to a pair of primers specific to ***mycobacterial*** species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of ***mycobacterial*** species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the ***mycobacterial*** species can be identified simply, economically, and accurately.

ST primer ***mycobacteria*** heat shock protein ***hsp65*** gene
IT Nucleic acid amplification (method)

(DNA; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial***

species)
 IT Heat-shock proteins
 RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (***HSP*** 65; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)
 IT Gene, microbial
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***HSP*** 65; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)
 IT Diagnosis
 (mol.; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)
 IT DNA sequences
 Mycobacterium
 Mycobacterium BCG
 Mycobacterium abscessus
 Mycobacterium africanum
 Mycobacterium aichiense
 Mycobacterium asiaticum
 Mycobacterium avium
 Mycobacterium avium paratuberculosis
 Mycobacterium bovis
 Mycobacterium celatum
 Mycobacterium chelonae
 Mycobacterium chitae
 Mycobacterium farcinogenes
 Mycobacterium flavescentes
 Mycobacterium fortuitum
 Mycobacterium gastri
 Mycobacterium genavense
 Mycobacterium gordonaee
 Mycobacterium haemophilum
 Mycobacterium interjectum
 Mycobacterium intracellulare
 Mycobacterium kansasii
 Mycobacterium leprae
 Mycobacterium malmoense
 Mycobacterium marinum
 Mycobacterium microti
 Mycobacterium mucogenicum
 Mycobacterium neoaurum
 Mycobacterium nonchromogenicum
 Mycobacterium parafortuitum
 Mycobacterium peregrinum
 Mycobacterium phlei
 Mycobacterium scrofulaceum
 Mycobacterium senegalense
 Mycobacterium shimoidei
 Mycobacterium simiae

Mycobacterium smegmatis
 Mycobacterium szulgai
 Mycobacterium terrae
 Mycobacterium thermoresistibile
 Mycobacterium triviale
 Mycobacterium tuberculosis
 Mycobacterium ulcerans
 Mycobacterium vaccae
 Mycobacterium wolinskyi
Nocardia carnea
 RFLP (restriction fragment length polymorphism)
Tsukamurella paurometabola
Tsukamurella pulmonis
Tsukamurella tyrosinosolvens
 (primers for amplifying ***mycobacterial*** heat shock protein
 HSP 65 gene and use for identifying ***mycobacterial***
 species)

IT Primers (nucleic acid)

RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)

 (primers for amplifying ***mycobacterial*** heat shock protein
 HSP 65 gene and use for identifying ***mycobacterial***
 species)

IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
 569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
 569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
 569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
 569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
 569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
 569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
 569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
 569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
 569432-52-6 569432-53-7 569432-54-8 569432-55-9

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

 (nucleotide sequence; primers for amplifying ***mycobacterial***
 heat shock protein ***HSP*** 65 gene and use for identifying
 mycobacterial species)

IT 569432-56-0

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

 (primer ***HSPF3*** sequence; primers for amplifying
 mycobacterial heat shock protein ***HSP*** 65 gene and use
 for identifying ***mycobacterial*** species)

IT 569432-57-1

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

 (primer ***HSPR3*** sequence; primers for amplifying
 mycobacterial heat shock protein ***HSP*** 65 gene and use
 for identifying ***mycobacterial*** species)

IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES

(Uses)
 (primers for amplifying ***mycobacterial*** heat shock protein
 HSP 65 gene and use for identifying ***mycobacterial***
 species)

IT 569477-29-8
 RL: PRP (Properties)
 (unclaimed sequence; primers for amplifying ***mycobacterial***
 heat shock protein ***HSP*** 65 gene and use for identifying
 mycobacterial species)

=> e kook yoon ho/au

E1	3	KOOK YOON BUM/AU
E2	1	KOOK YOON HAWN/AU
E3	4	--> KOOK YOON HO/AU
E4	291	KOOK YOON HOH/AU
E5	1	KOOK YOON HOH DR/AU
E6	1	KOOK YOON HOH*/AU
E7	10	KOOK YOON HWAN/AU
E8	3	KOOK YOON SANG/AU
E9	1	KOOK YOONAH/AU
E10	1	KOOK YOONBUM/AU
E11	1	KOOK YOONHO/AU
E12	14	KOOK YOONHOH/AU

=> s e1-e7 and mycobact? and HSP?
 L4 45 ("KOOK YOON BUM"/AU OR "KOOK YOON HAWN"/AU OR "KOOK YOON HO"/AU
 OR "KOOK YOON HOH"/AU OR "KOOK YOON HOH DR"/AU OR "KOOK YOON
 HOH*"/AU OR "KOOK YOON HWAN"/AU) AND MYCOBACT? AND HSP?

=> dup rem 14
 PROCESSING COMPLETED FOR L4
 L5 11 DUP REM L4 (34 DUPLICATES REMOVED)

=> d bib ab kwic 1-
 YOU HAVE REQUESTED DATA FROM 11 ANSWERS - CONTINUE? Y/(N):y

L5 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 1
 AN 2008:1298911 CAPLUS <<LOGINID::20090924>>
 DN 151:27682
 TI Proportions of ***Mycobacterium*** massiliense and
 Mycobacterium bolletii strains among Korean ***Mycobacterium***
 chelonae- ***Mycobacterium*** abscessus group isolates
 AU Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam
 Yong; Shim, Tae Sun; Kim, Bum-Joon; ***Kook, Yoon-Hoh***
 CS Department of Microbiology, Cancer Research Institute, Institute of
 Endemic Diseases, SNUMRC, and Clinical Research Institute, Seoul National
 University College of Medicine, Seoul National University Hospital, Seoul,
 110-799, S. Korea
 SO Journal of Clinical Microbiology (2008), 46(10), 3384-3390
 CODEN: JCMIDW; ISSN: 0095-1137
 PB American Society for Microbiology
 DT Journal
 LA English
 AB Korean isolates of the ***Mycobacterium*** chelonae-
 Mycobacterium abscessus group, which had been isolated from two
 different hospitals in South Korea, were identified by PCR restriction

anal. (PRA) and comparative sequence anal. of 16S rRNA genes, rpoB, and ***hsp65*** to evaluate the proportion of four closely related species (M. chelonae, M. abscessus, M. massiliense, and M. bolletii). Of the 144 rapidly growing ***mycobacterial*** strains tested, 127 strains (88.2%) belonged to the M. chelonae-M. abscessus group. In this group, M. chelonae, M. abscessus, M. massiliense, and M. bolletii accounted for 0.8% (n = 1), 51.2% (n = 65), 46.5% (n = 59), and 1.6% (n = 2), resp. Two isolates which showed discordant results, M. massiliense by rpoB sequence anal. and M. abscessus by ***hsp65*** sequence anal., were finally identified as M. massiliense based on the addnl. anal. of sodA and the 16S-23S internal transcribed spacer. M. abscessus group I isolates previously identified by ***hsp65*** PRA were all found to be M. abscessus, whereas group II isolates were further identified as M. massiliense or M. bolletii by sequencing of rpoB and ***hsp65*** . Smooth, rough, or mixed colonies of both M. abscessus and M. massiliense isolates were obsd. M. massiliense strains that were highly resistant to clarithromycin had a point mutation at the adenine at position 2058 (A2058) or 2059 (A2059) in the peptidyltransferase region of the 23S rRNA gene.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Proportions of ***Mycobacterium*** massiliense and ***Mycobacterium*** bolletii strains among Korean ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group isolates
AU Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam Yong; Shim, Tae Sun; Kim, Bum-Joon; ***Kook, Yoon-Hoh***
AB Korean isolates of the ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group, which had been isolated from two different hospitals in South Korea, were identified by PCR restriction anal. (PRA) and comparative sequence anal. of 16S rRNA genes, rpoB, and ***hsp65*** to evaluate the proportion of four closely related species (M. chelonae, M. abscessus, M. massiliense, and M. bolletii). Of the 144 rapidly growing ***mycobacterial*** strains tested, 127 strains (88.2%) belonged to the M. chelonae-M. abscessus group. In this group, M. chelonae, M. abscessus, M. . . . (n = 2), resp. Two isolates which showed discordant results, M. massiliense by rpoB sequence anal. and M. abscessus by ***hsp65*** sequence anal., were finally identified as M. massiliense based on the addnl. anal. of sodA and the 16S-23S internal transcribed spacer. M. abscessus group I isolates previously identified by ***hsp65*** PRA were all found to be M. abscessus, whereas group II isolates were further identified as M. massiliense or M. bolletii by sequencing of rpoB and ***hsp65*** . Smooth, rough, or mixed colonies of both M. abscessus and M. massiliense isolates were obsd. M. massiliense strains that were. . .
ST ***Mycobacterium*** antibiotic resistance clarithromycin taxonomy
IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(23 S; proportions of ***Mycobacterium*** massiliense and ***Mycobacterium*** bolletii strains among Korean ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group isolates)
IT Mutation
(point; proportions of ***Mycobacterium*** massiliense and ***Mycobacterium*** bolletii strains among Korean ***Mycobacterium*** chelonae- ***Mycobacterium*** abscessus group isolates)

IT Antibiotic resistance
Mycobacterium abscessus
Mycobacterium bolletii
Mycobacterium chelonae
Mycobacterium massiliense
(proportions of ***Mycobacterium*** massiliense and
Mycobacterium bolletii strains among Korean
Mycobacterium chelonae- ***Mycobacterium*** abscessus group
isolates)

IT 81103-11-9, Clarithromycin
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proportions of ***Mycobacterium*** massiliense and
Mycobacterium bolletii strains among Korean
Mycobacterium chelonae- ***Mycobacterium*** abscessus group
isolates)

L5 ANSWER 2 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 2

AN 2008:322988 BIOSIS <>LOGINID::20090924>>
DN PREV200800322987

TI ***Mycobacterium*** senuense sp nov., a slowly growing,
non-chromogenic species closely related to the ***Mycobacterium***
terrae complex.

AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil;
Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol and Immunol, Canc Res Inst,
Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (MAR
2008) Vol. 58, No. Part 3, pp. 641-646.
ISSN: 1466-5026.

DT Article
LA English
OS GenBank-DQ536407; EMBL-DQ536407; DDJB-DQ536407; GenBank-DQ536409;
EMBL-DQ536409; DDJB-DQ536409

ED Entered STN: 29 May 2008
Last Updated on STN: 29 May 2008

AB A previously undescribed, slowly growing, non-chromogenic
mycobacterium, isolated from a Korean patient with a symptomatic
pulmonary infection, is described as representing a novel species. Its
16S rRNA gene sequence was unique and phylogenetic analysis based on 16S
rRNA gene sequences showed that this organism belonged to the
Mycobacterium terrae subclade. Phenotypically, the strain was
generally similar to *M. terrae* and ***Mycobacterium***
nonchromogenicum, but its growth rate was slower than those of other *M.*
terrae complex strains. A unique mycolic acid profile and phylogenetic
analysis based on two different alternative chronometer molecules,
hsp65 and *rpoB*, confirm the taxonomic status of this strain as a
representative of a novel species. The name ***Mycobacterium***
senuense sp. nov. is proposed, with the type strain 05-832(T) (=DSM
44999(T) =KCTC 19147(T)).

TI ***Mycobacterium*** senuense sp nov., a slowly growing,
non-chromogenic species closely related to the ***Mycobacterium***
terrae complex.

AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil;
Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB A previously undescribed, slowly growing, non-chromogenic

mycobacterium , isolated from a Korean patient with a symptomatic pulmonary infection, is described as representing a novel species. Its 16S rRNA. . . gene sequence was unique and phylogenetic analysis based on 16S rRNA gene sequences showed that this organism belonged to the ***Mycobacterium*** terrae subclade. Phenotypically, the strain was generally similar to *M. terrae* and ***Mycobacterium*** nonchromogenicum, but its growth rate was slower than those of other *M. terrae* complex strains. A unique mycolic acid profile and phylogenetic analysis based on two different alternative chronometer molecules, ***hsp65*** and *rpoB*, confirm the taxonomic status of this strain as a representative of a novel species. The name ***Mycobacterium*** senuense sp. nov. is proposed, with the type strain 05-832(T) (=DSM 44999(T) =KCTC 19147(T)).

IT Major Concepts
Population Genetics (Population Studies); Systematics and Taxonomy
IT Chemicals & Biochemicals
rpoB; ***hsp65*** ; 16S ribosomal RNA [16S rRNA, gene sequence]
ORGN . . .
Chordata; Animalia
Organism Name
human (common): aged, host, Korean, male
Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Mycobacteriaceae *08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium terrae (species)
Mycobacterium nonchromogenicum (species)
Mycobacterium senuense (species): new species, description,
strain-05-832-T
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L5 ANSWER 3 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 3
AN 2008:636733 BIOSIS <>LOGINID::20090924>>
DN PREV200800636732
TI Differentiation of ***mycobacteria*** in sputa by duplex polymerase
chain reaction for ***mycobacterial*** ***hsp65*** gene.
AU Kim, Bum-Joon [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong;
Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Eui-Chong; Joo, Sei Ick;
Lee, Jae Seok; Yim, Jae-Joon
CS Seoul Natl Univ, Coll Med, Canc Res Inst, Dept Microbiol and Immunol,
Seoul 110744, South Korea
kbumjoon@snu.ac.kr; yimjj@snu.ac.kr
SO Diagnostic Microbiology and Infectious Disease, (OCT 2008) Vol. 62, No. 2,
pp. 193-198.
CODEN: DMIDDZ. ISSN: 0732-8893.
DT Article
LA English
ED Entered STN: 19 Nov 2008
Last Updated on STN: 19 Nov 2008
AB Early differentiation of ***mycobacteria*** in Sputa is crucial. This
study was set to evaluate the usefulness of a newly developed duplex

polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating ***mycobacteria*** in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. ***Mycobacterial*** species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of ***mycobacterial*** species were made based on 1) results of species identification based on ***mycobacterial*** colonies or 2) results of species identification of other sputa from the same patients and clinical findings. The duplex PCR-based method correctly identified 83.2% Sputa from tuberculosis patients and 82.2% sputa from nontuberculous ***mycobacteria*** patients, whereas the colonybased method correctly identified 86.1% and 77.8%, respectively. Sensitivity and specificity of the colony-based method for ***Mycobacterium*** tuberculosis were 86.1% and 100%, respectively, whereas those of the duplex PCR-based method were 83.2% and 95.6%, respectively. The duplex PCR-based method, to differentiate ***mycobacterial*** species in Sputa, produced comparable results as those of the colony-based identification method. (C) 2008 Elsevier Inc. All rights reserved.

TI Differentiation of ***mycobacteria*** in sputa by duplex polymerase chain reaction for ***mycobacterial*** ***hsp65*** gene.
AU Kim, Bum-Joon [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Eui-Chong; Joo, Sei Ick; Lee, Jae Seok; Yim, Jae-Joon
AB Early differentiation of ***mycobacteria*** in Sputa is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating ***mycobacteria*** in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. ***Mycobacterial*** species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of ***mycobacterial*** species were made based on 1) results of species identification based on ***mycobacterial*** colonies or 2) results of species identification of other sputa from the same patients and clinical findings. The duplex PCR-based method correctly identified 83.2% Sputa from tuberculosis patients and 82.2% sputa from nontuberculous ***mycobacteria*** patients, whereas the colonybased method correctly identified 86.1% and 77.8%, respectively. Sensitivity and specificity of the colony-based method for ***Mycobacterium*** tuberculosis were 86.1% and 100%, respectively, whereas those of the duplex PCR-based method were 83.2% and 95.6%, respectively. The duplex PCR-based method, to differentiate ***mycobacterial*** species in Sputa, produced comparable results as those of the colony-based identification method. (C) 2008 Elsevier Inc. All rights reserved.

IT Major Concepts
Methods and Techniques; Infection; Molecular Genetics (Biochemistry and Molecular Biophysics); Human Medicine (Medical Sciences)

IT Diseases
Mycobacterium infection: bacterial disease, diagnosis

ORGN . . .
Primates; Mammalia; Vertebrata; Chordata; Animalia
Organism Name
human (common): host

Taxa Notes

Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier

Mycobacteriaceae 08881

Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms

Organism Name

Mycobacterium	tuberculosis (species): pathogen
Mycobacterium	abscessus (species): pathogen
Mycobacterium	avium (species): pathogen
Mycobacterium	intracellulare (species): pathogen
Mycobacterium	fortuitum (species): pathogen
Mycobacterium	chelonae (species): pathogen
Mycobacterium	kansasii (species): pathogen
Mycobacterium	parascrofulaceum (species): pathogen

Taxa Notes

Bacteria, Eubacteria, Microorganisms
GEN ***Mycobacterium*** ***hsp65*** gene (***Mycobacteriaceae***)

L5 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 4

AN 2007:1135732 CAPLUS <<LOGINID::20090924>>

DN 148:281748

TI Outbreak of ***Mycobacterium*** massiliense infection associated with intramuscular injections

AU Kim, Hee-Youn; Yun, Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; Kim, Bum-Joon; ***Kook, Yoon-Hoh***

CS Department of Microbiology, Cancer Research Institute, Institute of Endemic Diseases, SNUMRC, S. Korea

SO Journal of Clinical Microbiology (2007), 45(9), 3127-3130
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB Twelve strains of a rapidly growing ***Mycobacterium*** species were isolated from an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65*** . These isolates were identified as ***Mycobacterium*** massiliense (100% similarity).

OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Outbreak of ***Mycobacterium*** massiliense infection associated with intramuscular injections

AU . . . Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; Kim, Bum-Joon; ***Kook,***
*** Yoon-Hoh***

AB Twelve strains of a rapidly growing ***Mycobacterium*** species were isolated from an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65*** . These isolates were identified as ***Mycobacterium*** massiliense (100% similarity).

ST ***Mycobacterium*** infection ribostamycin intramuscular injection antibiotic susceptibility; gene sequence rpoB ***hsp65***
Mycobacterium infection taxonomy epidemiol

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)
(***HSP*** 65, gene ***hsp65*** ; outbreak of
Mycobacterium massiliense infection assocd. with i.m.
injections)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(***hsp65*** ; outbreak of ***Mycobacterium*** massiliense
infection assocd. with i.m. injections)

IT Bacterial infection
(i.m. injection-assocd. infection; outbreak of ***Mycobacterium***
massiliense infection assocd. with i.m. injections)

IT Pharmaceutical injections
(i.m. injections, i.m. injection-assocd. infection; outbreak of
Mycobacterium massiliense infection assocd. with i.m.
injections)

IT Evolution
(mol., rpoB and ***hsp65*** sequence phylogeny; outbreak of
Mycobacterium massiliense infection assocd. with i.m.
injections)

IT Epidemiology
Taxonomy
(mol.; outbreak of ***Mycobacterium*** massiliense infection
assocd. with i.m. injections)

IT Antibiotic resistance
DNA sequences
Mycobacterium abscessus
Mycobacterium aichiense
Mycobacterium hassiacum
Mycobacterium massiliense
Mycobacterium parafortuitum

Protein sequences
(outbreak of ***Mycobacterium*** massiliense infection assocd. with
i.m. injections)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(rpoB; outbreak of ***Mycobacterium*** massiliense infection
assocd. with i.m. injections)

IT 564-25-0, Doxycycline 10118-90-8, Minocycline 37517-28-5, Amikacin
81103-11-9, Clarithromycin 83905-01-5, Azithromycin
RL: BSU (Biological study, unclassified); PAC (Pharmacological activity);
THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(***Mycobacterium*** susceptibility; outbreak of
Mycobacterium massiliense infection assocd. with i.m.
injections)

IT 1007444-81-6 1007444-83-8 1007444-85-0 1007444-87-2 1007444-89-4
1008181-63-2 1008181-65-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; outbreak of ***Mycobacterium*** massiliense
infection assocd. with i.m. injections)

IT 53797-35-6, Ribostamycin sulfate
RL: ADV (Adverse effect, including toxicity); PAC (Pharmacological
activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(i.m. injection-assocd. infection; outbreak of ***Mycobacterium***
massiliense infection assocd. with i.m. injections)

IT 1007444-80-5 1007444-82-7 1007444-84-9 1007444-86-1 1007444-88-3
1008181-62-1 1008181-64-3
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(nucleotide sequence; outbreak of ***Mycobacterium*** massiliense
infection assocd. with i.m. injections)

IT 9014-24-8, RNA polymerase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(.beta. subunit, gene rpoB; outbreak of ***Mycobacterium***
massiliense infection assocd. with i.m. injections)

L5 ANSWER 5 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 5

AN 2007:338789 BIOSIS <>LOGINID::20090924>>

DN PREV200700342042

TI ***Mycobacterium*** seoulense sp nov., a slowly growing
scotochromogenic species.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu,
Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ;
Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Dept Microbiol and Immunol, Canc Res Inst, Coll Med,
Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (MAR
2007) Vol. 57, No. Part 3, pp. 594-599.
ISSN: 1466-5026.

DT Article

LA English

ED Entered STN: 6 Jun 2007
Last Updated on STN: 6 Jun 2007

AB A. previously undescribed, slowly growing, scotochromogenic
mycobacterium was isolated from a patient with symptomatic
pulmonary infection during ***hsp65*** sequence-based identification
of Korean clinical isolates. Phenetic characteristics of this strain were
generally similar to those of ***Mycobacterium*** nebraskense and
Mycobacterium scrofulaceum. However, some phenetic
characteristics differentiated it from these two species. Its 16S rRNA
gene sequences were unique and phylogenetic analysis based on 16S rRNA
gene sequences placed the organism in the slowly growing
Mycobacterium group close to M. nebraskense and M. scrofulaceum.
Its unique rnycolic acid profiles and the results of phylogenetic analysis
based on two independent alternative chronometer molecules, ***hsp65***
and rpoB, confirmed the taxonomic status of this strain as representing a
novel species. These data support the conclusion that this strain
represents a novel ***mycobacterial*** species, for which the name
Mycobacterium seoulense sp. nov. is proposed. The type strain is
strain 03-19(T) (=DSM 44998(T)=KCTC 19146(T)).

TI ***Mycobacterium*** seoulense sp nov., a slowly growing
scotochromogenic species.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu,
Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ;
Kim, Bum-Joon [Reprint Author]

AB A. previously undescribed, slowly growing, scotochromogenic
mycobacterium was isolated from a patient with symptomatic
pulmonary infection during ***hsp65*** sequence-based identification
of Korean clinical isolates. Phenetic characteristics of this strain were

generally similar to those of ***Mycobacterium*** nebraskense and ***Mycobacterium*** scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic analysis based on 16S rRNA gene sequences placed the organism in the slowly growing ***Mycobacterium*** group close to M. nebraskense and M. scrofulaceum. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel ***mycobacterial*** species, for which the name ***Mycobacterium*** seoulense sp. nov. is proposed. The type strain is strain 03-19(T) (=DSM 44998(T)=KCTC 19146(T)).

IT . . .
Medicine (Human Medicine, Medical Sciences); Systematics and Taxonomy
IT Parts, Structures, & Systems of Organisms
lung: respiratory system
IT Diseases
 Mycobacterium infection: bacterial disease, infectious disease, genetics
IT Diseases
 pulmonary infection: respiratory system disease, infectious disease, bacterial disease, symptom, genetics
 Respiratory Tract. . .
ORGN . . .
Animalia
Organism Name
human (common): middle age, host, Korean, female
Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
 Mycobacteriaceae *08881
Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
Organism Name
 Mycobacterium leprae (species): pathogen
 Mycobacterium tuberculosis (species): pathogen
 Mycobacterium marinum (species): pathogen
 Mycobacterium haemophilum (species): pathogen
 Mycobacterium ulcerans (species): pathogen
 Mycobacterium intracellulare (species): pathogen, strain-
ATCC 13950
 Mycobacterium seoulense (species): new species, pathogen, description, rod-shaped, bent cell, strain-03-19, strain-DSM 44998, strain-KCTC 19146
 Mycobacterium nebraskense (species): pathogen, strain-YNMC-
MY 1349
 Mycobacterium scrofulaceum (species): pathogen, strain-DSM 43992
 Mycobacterium avium (species): pathogen, strain-DSM 44156
 Mycobacterium (genus): pathogen, strain-IWGMT 90160
 Mycobacterium gastri (species): pathogen, strain-ATCC 15754
 Mycobacterium kansasii (species): pathogen, strain-ATCC

Mycobacterium paratuberculosis (species): pathogen,
strain-ATCC 19698
 malmoense (species): pathogen, strain-ATCC
29571
 szulgai (species): pathogen, strain-ATCC 35799
 simiae (species): pathogen, strain-ATCC 25275

Taxa Notes
Bacteria, Eubacteria, Microorganisms

ORGN Classifier
Nocardioform Actinomycetes 08810

Super Taxa
Actinomycetes and Related. . .

GEN ***Mycobacterium*** ***hsp65*** gene [***Mycobacterium*** heat
shock protein 65 gene] (***Mycobacteriaceae***): expression;
 rpoB gene (***Mycobacteriaceae***): expression

L5 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:465634 CAPLUS <>LOGINID::20090924>>
DN 147:339410

TI ***Mycobacterium*** seoulense sp. nov., a slowly growing
scotochromogenic species

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu,
Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ;
Kim, Bum-Joon

CS Department of Microbiology and Immunology, Cancer Research Institute and
Liver Research Institute, College of Medicine, Seoul National University,
Seoul, 110-799, S. Korea

SO International Journal of Systematic and Evolutionary Microbiology (2007),
57(3), 593-599

PB CODEN: ISEMF5; ISSN: 1466-5026

PB Society for General Microbiology

DT Journal

LA English

AB A previously undescribed, slowly growing, scotochromogenic
mycobacterium was isolated from a patient with symptomatic
pulmonary infection during ***hsp65*** sequence-based identification
of Korean clin. isolates. Phenetic characteristics of this strain were
generally similar to those of ***Mycobacterium*** nebraskense and
Mycobacterium scrofulaceum. However, some phenetic
characteristics differentiated it from these two species. Its 16S rRNA
gene sequences were unique and phylogenetic anal. based on 16S rRNA gene
sequences placed the organism in the slowly growing ***Mycobacterium***
group close to M. nebraskense and M. scrofulaceum. Its unique mycolic
acid profiles and the results of phylogenetic anal. based on two
independent alternative chronometer mols., ***hsp65*** and rpoB,
confirmed the taxonomic status of this strain as representing a novel
species. These data support the conclusion that this strain represents a
novel ***mycobacterial*** species, for which the name
Mycobacterium seoulense sp. nov. is proposed. The type strain is
strain 03-19T (= DSM 44998T = KCTC 19146T).

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***Mycobacterium*** seoulense sp. nov., a slowly growing
scotochromogenic species

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu,
Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ;
Kim, Bum-Joon

AB A previously undescribed, slowly growing, scotochromogenic ***mycobacterium*** was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of ***Mycobacterium*** nebraskense and ***Mycobacterium*** scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic anal. based on 16S rRNA gene sequences placed the organism in the slowly growing ***Mycobacterium*** group close to M. nebraskense and M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel ***mycobacterial*** species, for which the name ***Mycobacterium*** seoulense sp. nov. is proposed. The type strain is strain 03-19T (= DSM 44998T = KCTC 19146T).

ST ***Mycobacterium*** scotochromogenic 16S rRNA gene rpoB ***hsp65***

IT rRNA

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(16 S; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(16S rRNA; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** 65; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT DNA sequences

Human

 Mycobacterium seoulense

Protein sequences
(***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***hsp65*** ; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT Evolution

(mol., phylogeny; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT Taxonomy

(mol.; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(rpoB; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT 9014-24-8, RNA polymerase

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT 948634-47-7 948634-50-2
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

IT 948634-46-6 948634-48-8 948634-49-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; ***Mycobacterium*** seoulense sp. nov., a slowly growing scotochromogenic species)

L5 ANSWER 7 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 6

AN 2007:135186 BIOSIS <>LOGINID::20090924>>

DN PREV200700134974

TI Direct application of AvaII PCR restriction fragment length polymorphism analysis (AvaII PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai, Gil-Han; Do, Junghwan; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO Microbiology and Immunology, (2007) Vol. 51, No. 1, pp. 105-110.
CODEN: MIIMDV. ISSN: 0385-5600.

DT Article

LA English

ED Entered STN: 22 Feb 2007
Last Updated on STN: 22 Feb 2007

AB To evaluate the usefulness of the AvaII PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic ***mycobacteria*** from clinical specimens, we applied this method to

40 sputum samples and compared the results to those obtained by IS6110 PCR. Although this method showed a sensitivity slightly lower than IS6110 PCR (97.5% vs. 100%), it detected infections of M. avium complex (MAC) in two patients, which was not possible by IS6110 PCR. We conclude that Avall PRA is a highly effective method for directly detecting pathogenic ***mycobacteria*** in primary clinical specimens.

TI Direct application of AvaII PCR restriction fragment length polymorphism analysis (AvaII PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai, Gil-Han; Do, Junghwan; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB To evaluate the usefulness of the AvaII PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic ***mycobacteria*** from clinical specimens, we applied this method to

40 sputum samples and compared the results to those obtained by IS6110. . . was not possible by IS6110 PCR. We conclude that Avall PRA is a highly effective method for directly detecting pathogenic ***mycobacteria***

in primary clinical specimens.

IT . . .
Infection; Methods and Techniques; Molecular Genetics (Biochemistry and
Molecular Biophysics)

IT Parts, Structures, & Systems of Organisms
sputum

IT Diseases
Mycobacterium avium infection: bacterial disease, infectious
disease

IT Diseases
Mycobacterium tuberculosis infection: bacterial disease,
infectious disease

IT Chemicals & Biochemicals
644 bp

ORGN . . .
Primates; Mammalia; Vertebrata; Chordata; Animalia

Organism Name
human (common): host

Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium tuberculosis (species): pathogen
Mycobacterium avium (species): pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** avium ***hsp65*** gene [***Mycobacterium***
avium heat shock protein 65 gene] (***Mycobacteriaceae***):
expression; ***Mycobacterium*** tuberculosis ***hsp65*** gene [
Mycobacterium tuberculosis heat shock protein 65 gene] (
Mycobacteriaceae): expression

L5 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 7
AN 2006:1304935 CAPLUS <>LOGINID::20090924>>
DN 146:515458
TI Differentiation of ***mycobacterial*** species by ***hsp65***
duplex PCR followed by duplex-PCR-based restriction analysis and direct
sequencing
AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai,
Gill-Han; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim,
Bum-Joon
CS Department of Microbiology and Immunology, Cancer Research Institute and
Liver Research Institute, College of Medicine, Seoul National University,
Seoul, 110-799, S. Korea
SO Journal of Clinical Microbiology (2006), 44(11), 3855-3862
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Here we describe a novel duplex PCR method which can differentiate
Mycobacterium tuberculosis and nontuberculosis
mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of
different sizes (195 and 515 bp, resp.). The devised technique was

applied to 54 ref. and 170 clin. isolates and differentiated all strains into their resp. groups with 100% sensitivity and specificity. Furthermore, a duplex PCR-restriction anal. (duplex PRA) and a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and subspecies levels by subsequent procedures (PRA or direct sequencing) targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for identifying ***mycobacterial*** culture isolates at the species level.

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon

AB Here we describe a novel duplex PCR method which can differentiate ***Mycobacterium*** tuberculosis and nontuberculosis ***mycobacteria*** (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin.. . . a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and. . . targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for identifying ***mycobacterial*** culture isolates at the species level.

ST ***Mycobacterium*** species differentiation ***hsp65*** duplex PCR restriction analysis sequencing

IT DNA sequence analysis

Mycobacterium tuberculosis

Tuberculosis

(differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Primers (nucleic acid)

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Genetic methods

(duplex-PCR-based restriction anal.; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Polymerase chain reaction

(duplex; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)

IT Gene, microbial

RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; differentiation of ***mycobacterial*** species by
hsp65 duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)

IT Human
(isolates from; differentiation of ***mycobacterial*** species by
hsp65 duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)

IT Diagnosis
(mol.; differentiation of ***mycobacterial*** species by
hsp65 duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)

IT ***Mycobacterium***
(nontuberculosis; differentiation of ***mycobacterial*** species by
hsp65 duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)

IT 936858-56-9 936858-57-0 936858-58-1 936858-59-2 936858-60-5
936858-61-6 936858-62-7 936858-64-9 936858-65-0

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; differentiation of ***mycobacterial*** species by
hsp65 duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)

L5 ANSWER 9 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 8

AN 2005:448449 BIOSIS <>LOGINID::20090924>>

DN PREV200510237956

TI Differentiation of ***Mycobacterium*** species by analysis of the heat-shock protein 65 gene (***hsp65***).

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; ***Kook,*** *** Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (JUL 2005) Vol. 55, No. Part 4, pp. 1649-1656.
ISSN: 1466-5026.

DT Article

LA English

ED Entered STN: 3 Nov 2005
Last Updated on STN: 3 Nov 2005

AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 ***Mycobacterium*** strains containing 56 reference ***Mycobacterium*** species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between ***Mycobacterium*** species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene, thus revealing natural relationships among

Mycobacterium species. When a direct sequencing protocol targeting 422 bp sequences was applied to 70 non-tuberculous ***mycobacterium*** (NTM) clinical isolates, all NTMs were clearly identified. In addition, an Xhol PCR restriction fragment length polymorphism analysis method for the differentiation of ***Mycobacterium***, tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of ***mycobacteria***.

TI Differentiation of ***Mycobacterium*** species by analysis of the heat-shock protein 65 gene (***hsp65***).

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; ***Kook,*** Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 ***Mycobacterium*** strains containing 56 reference ***Mycobacterium*** species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between ***Mycobacterium*** species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene, thus revealing natural relationships among ***Mycobacterium*** species. When a direct sequencing protocol targeting 422 bp sequences was applied to 70 non-tuberculous ***mycobacterium*** (NTM) clinical isolates, all NTMs were clearly identified. In addition, an Xhol PCR restriction fragment length polymorphism analysis method for the differentiation of ***Mycobacterium***, tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of ***mycobacteria***.

IT . . . Genetics (Population Studies); Systematics and Taxonomy

IT Chemicals & Biochemicals 16S rRNA [16S ribosomal RNA]; endonuclease; heat shock protein 65 [***HSP65***]

ORGN Classifier ***Mycobacteriaceae*** 08881

Super Taxa ***Mycobacteria*** ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms

Organism Name ***Mycobacterium*** tuberculosis (species)
Mycobacterium (genus)

Taxa Notes Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** 16S rRNA gene (***Mycobacteriaceae***); ***Mycobacterium*** ***hsp65*** gene [***Mycobacterium*** heat-shock protein 65 gene gene] (***Mycobacteriaceae***)

L5 ANSWER 10 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 9

AN 2005:437869 BIOSIS <>LOGINID::20090924>>

DN PREV200510224308

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm

targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of ***Mycobacterium*** spp.

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO Journal of Microbiological Methods, (AUG 2005) Vol. 62, No. 2, pp. 199-209.
CODEN: JMIMDQ. ISSN: 0167-7012.

DT Article

LA English

ED Entered STN: 26 Oct 2005
Last Updated on STN: 26 Oct 2005

AB A method based on PCR-restriction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of ***mycobacteria*** to the species level. A 644 bp region of ***hsp65*** in 62 ***mycobacteria*** reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, Avall, HphI, and HpaII. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the separation of M avium, M intracellulare and M tuberculosis to the species level by Avall digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clinical isolates, which had been characterized by conventional biochemical testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of ***mycobacteria*** culture isolates at the species level. (c) 2005 Elsevier B.V. All rights reserved.

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of ***Mycobacterium*** spp.

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB A method based on PCR-restriction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of ***mycobacteria*** to the species level. A 644 bp region of ***hsp65*** in 62 ***mycobacteria*** reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, Avall, HphI, and HpaII. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the separation of . . . biochemical testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of ***mycobacteria*** culture isolates at the species level. (c) 2005 Elsevier B.V. All rights reserved.

ORGN . . .
Organisms 08800
Super Taxa
Eubacteria; Bacteria; Microorganisms
Organism Name
Tsukamurella paurometabola (species): pathogen

Taxa Notes

Bacteria, Eubacteria, Microorganisms

ORGN Classifier

Mycobacteriaceae 08881

Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms;

Eubacteria; Bacteria; Microorganisms

Organism Name

Mycobacterium tuberculosis (species): pathogen

Mycobacterium avium (species): pathogen

Mycobacterium intracellulare (species): pathogen

Mycobacterium (genus): pathogen, 62 species

Taxa Notes

Bacteria, Eubacteria, Microorganisms

ORGN Classifier

Nocardioform Actinomycetes 08810

Super Taxa

Actinomycetes and Related Organisms; . . .

GEN ***Mycobacterium*** ***hsp65*** gene [***Mycobacterium*** heat shock protein 65 gene] (***Mycobacteriaceae***)

L5 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2003:591378 CAPLUS <>LOGINID::20090924>>

DN 139:146183

TI Primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species

IN Kim, Bum-joon; ***Kook, Yoon-ho*** ; Kim, Jeong-mi

PA Biomedlab Corporation, S. Korea

SO PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305
	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB The present invention relates to a pair of primers specific to ***mycobacterial*** species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of

mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the ***mycobacterial*** species can be identified simply, economically, and accurately.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species

IN Kim, Bum-joon; ***Kook, Yoon-ho*** ; Kim, Jeong-mi

AB The present invention relates to a pair of primers specific to ***mycobacterial*** species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of ***mycobacterial*** species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the ***mycobacterial*** species can be identified simply, economically, and accurately.

ST primer ***mycobacteria*** heat shock protein ***hsp65*** gene
IT Nucleic acid amplification (method)

(DNA; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

IT Heat-shock proteins

RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)

(***HSP*** 65; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

IT Gene, microbial

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(***HSP*** 65; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

IT Diagnosis

(mol.; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

IT DNA sequences

Mycobacterium
Mycobacterium BCG

Mycobacterium abscessus
 Mycobacterium africanum
 Mycobacterium aichiense
 Mycobacterium asiaticum
 Mycobacterium avium
 Mycobacterium avium paratuberculosis
 Mycobacterium bovis
 Mycobacterium celatum
 Mycobacterium chelonae
 Mycobacterium chitae
 Mycobacterium farcinogenes
 Mycobacterium flavesrens
 Mycobacterium fortuitum
 Mycobacterium gastri
 Mycobacterium genavense
 Mycobacterium gordonaee
 Mycobacterium haemophilum
 Mycobacterium interjectum
 Mycobacterium intracellulare
 Mycobacterium kansasii
 Mycobacterium leprae
 Mycobacterium malmoense
 Mycobacterium marinum
 Mycobacterium microti
 Mycobacterium mucogenicum
 Mycobacterium neoaurum
 Mycobacterium nonchromogenicum
 Mycobacterium parafortuitum
 Mycobacterium peregrinum
 Mycobacterium phlei
 Mycobacterium scrofulaceum
 Mycobacterium senegalense
 Mycobacterium shimoidei
 Mycobacterium simiae
 Mycobacterium smegmatis
 Mycobacterium szulgai
 Mycobacterium terrae
 Mycobacterium thermoresistibile
 Mycobacterium triviale
 Mycobacterium tuberculosis
 Mycobacterium ulcerans
 Mycobacterium vaccae
 Mycobacterium wolinskyi

Nocardia carnea

RFLP (restriction fragment length polymorphism)

Tsukamurella paurometabola

Tsukamurella pulmonis

Tsukamurella tyrosinosolvens

(primers for amplifying ***mycobacterial*** heat shock protein
 HSP 65 gene and use for identifying ***mycobacterial***
 species)

IT Primers (nucleic acid)

RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)

(primers for amplifying ***mycobacterial*** heat shock protein

HSP 65 gene and use for identifying ***mycobacterial*** species)

IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
 569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
 569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
 569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
 569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
 569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
 569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
 569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
 569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
 569432-52-6 569432-53-7 569432-54-8 569432-55-9

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(nucleotide sequence; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

IT 569432-56-0

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(primer ***HSPF3*** sequence; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

IT 569432-57-1

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(primer ***HSPR3*** sequence; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

IT 569477-29-8

RL: PRP (Properties)

(unclaimed sequence; primers for amplifying ***mycobacterial*** heat shock protein ***HSP*** 65 gene and use for identifying ***mycobacterial*** species)

=> e kim jeong mi/au

E1	1	KIM JEONG MANN/AU
E2	30	KIM JEONG MEE/AU
E3	150	--> KIM JEONG MI/AU
E4	478	KIM JEONG MIN/AU
E5	2	KIM JEONG MM/AU
E6	15	KIM JEONG MO/AU
E7	4	KIM JEONG MOG/AU
E8	40	KIM JEONG MOK/AU
E9	1	KIM JEONG MONG/AU
E10	16	KIM JEONG MOOG/AU
E11	5	KIM JEONG MOOK/AU

E12 3 KIM JEONG MOON/AU

=> s e3 and mycobact? and HSP?
L6 1 "KIM JEONG MI"/AU AND MYCOBACT? AND HSP?

=> d

L6 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:591378 CAPLUS <<LOGINID::20090924>>
DN 139:146183
TI Primers for amplifying ***mycobacterial*** heat shock protein
 HSP 65 gene and use for identifying ***mycobacterial***
 species

IN Kim, Bum-joon; Kook, Yoon-ho; ***Kim, Jeong-mi***
PA Biomedlab Corporation, S. Korea
SO PCT Int. Appl., 102 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305
	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s (HSP 65) and mycobact? and primer?
L7 47 (HSP 65) AND MYCOBACT? AND PRIMER?

=> dup rem 17
PROCESSING COMPLETED FOR L7
L8 42 DUP REM L7 (5 DUPLICATES REMOVED)

=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 42 ANSWERS - CONTINUE? Y/(N):y

L8 ANSWER 1 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2009:970747 CAPLUS <<LOGINID::20090924>>

TI Method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis

IN Kim, Beom Jun; Park, Ju Hui

PA Seoul National University, R & Db Foundation, S. Korea

SO Repub. Korean Kongkae Taeho Kongbo, 13pp.

CODEN: KRXXA7

DT Patent

LA Korean

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 2009085350	A	20090807	KR 2008-11190	20080204
PRAI	KR 2008-11190		20080204		

AB This invention provided a method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing. The primers were used for amplifying 1623 bp HSP65 gene and the signature nucleotide at position 423 (G), 424 (C) and 701 (C) were further identified by DNA sequencing. The method provided in this invention can be used for identifying the nontuberculous ***Mycobacteria*** from sputum without culturing the ***Mycobacteria*** .

TI Method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis

AB This invention provided a method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing. The primers were used for amplifying 1623 bp HSP65 gene and the signature nucleotide at position . . . (C) were further identified by DNA sequencing. The method provided in this invention can be used for identifying the nontuberculous ***Mycobacteria*** from sputum without culturing the ***Mycobacteria*** .

ST detection nontuberculous ***Mycobacteria*** nested PCR direct sequencing ***primer***

IT Heat-shock proteins

RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(***HSP*** ***65*** , gene for; method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis)

IT Genetic methods

Sputum

Test kits

(method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis)

IT ***Primers*** (nucleic acid)

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis)

IT Diagnosis

(mol.; method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis)

IT DNA sequence analysis

(nested PCR-direct sequencing; method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use

for diagnosis)

IT Polymerase chain reaction

(nested, nested PCR-direct sequencing; method for detection of

nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis)
 IT ***Mycobacterium***
 (nontuberculous ***Mycobacteria*** ; method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis)
 IT Gene, microbial
 RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (test kit for; method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis)
 IT 1185959-99-2 1185960-00-2 1185960-01-3 1185960-02-4
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (nucleotide sequence; method for detection of nontuberculous ***Mycobacteria*** using nested PCR-direct sequencing and its use for diagnosis)
 L8 ANSWER 2 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2009:716844 CAPLUS <>LOGINID::20090924>>
 DN 151:121975
 TI Preparation of fusion protein containing ***Mycobacterium*** tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis
 IN Xiong, Sidong; Gao, Haifeng; Xu, Wei
 PA Fudan University, Peop. Rep. China
 SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 39pp.
 CODEN: CNXXEV
 DT Patent
 LA Chinese
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CN 101451145	A	20090610	CN 2007-10171416	20071130
PRAI	CN 2007-10171416		20071130		
AB	The title gene vaccine, as a vector, comprises the full-length gene sequence of ***Mycobacterium*** tuberculosis heat shock protein HSP65, and the genes of four T-cell epitope peptides derived from ***Mycobacterium*** tuberculosis antigens. This invention provides a process of prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis heat shock protein HSP65 and four epitopes. The epitopes were selected 189th-228th residues of ***Mycobacterium*** tuberculosis ESAT-6 protein, the 369th-405th residues of ***Mycobacterium*** tuberculosis Ag85A protein, the 162nd-207th residues of ***Mycobacterium*** tuberculosis CFP-10 protein, and the 141st-153th residues of ***Mycobacterium*** tuberculosis Ag85B protein. The fusion protein induced cellular immunostimulation of T cells. The fusion protein can be use for preventing and treating tuberculosis.				
TI	Preparation of fusion protein containing ***Mycobacterium*** tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis				
AB	The title gene vaccine, as a vector, comprises the full-length gene sequence of ***Mycobacterium*** tuberculosis heat shock protein HSP65, and the genes of four T-cell epitope peptides derived from				

Mycobacterium tuberculosis antigens. This invention provides a process of prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis heat shock protein HSP65 and four epitopes. The epitopes were selected 189th-228th residues of ***Mycobacterium*** tuberculosis ESAT-6 protein, the 369th-405th residues of ***Mycobacterium*** tuberculosis Ag85A protein, the 162nd-207th residues of ***Mycobacterium*** tuberculosis CFP-10 protein, and the 141st-153th residues of ***Mycobacterium*** tuberculosis Ag85B protein. The fusion protein induced cellular immunostimulation of T cells. The fusion protein can be used for preventing. . .

ST fusion ***Mycobacterium*** heat shock protein HSP65 T cell epitope; DNA protein sequence fusion protein

IT Antigens
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(85A, fusion protein with ESAT-6 fragment, HSP65, CFP-10 protein fragment; prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis)

IT Proteins
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(CFP-10, fusion protein with HSP65, ESAT-6 and Ag85A protein fragments; prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis)

IT Proteins
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(ESAT-6, fusion protein with HSP65, Ag85A protein CFP-10 protein fragments; prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis)

IT Heat-shock proteins
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(***HSP*** ***65*** , fusion protein with ESAT-6 protein, Ag85A protein CFP-10 protein fragments; prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis)

IT Immunostimulation
(cellular; prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis)

IT Fusion proteins (chimeric proteins)
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(comprising HSP65, ESAT-6 protein, Ag85A protein CFP-10 protein fragments; prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis)

IT Chimeric gene
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(for fusion protein; prepn. of fusion protein contg.
Mycobacterium tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis)

IT Genetic vectors
 (pVAX1; prepn. of fusion protein contg. ***Mycobacterium***
 tuberculosis heat shock protein HSP65 and T-cell epitopes and its use
 as vaccine for treatment of tuberculosis)

IT Genetic vectors
 (pcDNA3.1; prepn. of fusion protein contg. ***Mycobacterium***
 tuberculosis heat shock protein HSP65 and T-cell epitopes and its use
 as vaccine for treatment of tuberculosis)

IT Drug delivery systems
Epitopes
Genetic engineering
Immunotherapy
 Mycobacterium tuberculosis
T cell
Tuberculosis
Tuberculostatics
Vaccines
 (prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis
 heat shock protein HSP65 and T-cell epitopes and its use as vaccine for
 treatment of tuberculosis)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); PRP
(Properties); ANST (Analytical study); BIOL (Biological study); USES
(Uses)
 (prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis
 heat shock protein HSP65 and T-cell epitopes and its use as vaccine for
 treatment of tuberculosis)

IT Gene, microbial
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES
(Uses)
 (prepn. of fusion protein contg. ***Mycobacterium*** tuberculosis
 heat shock protein HSP65 and T-cell epitopes and its use as vaccine for
 treatment of tuberculosis)

IT 1151428-73-7P 1151431-92-3P 1152052-53-3P 1169389-53-0P
1169721-42-9P 1169721-43-0P
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (amino acid sequence; prepn. of fusion protein contg.
 Mycobacterium tuberculosis heat shock protein HSP65 and T-cell
 epitopes and its use as vaccine for treatment of tuberculosis)

IT 1169721-45-2 1169721-46-3 1169721-47-4 1169721-48-5 1169721-49-6
1169721-50-9 1169721-51-0 1169721-52-1 1169721-53-2
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (nucleotide sequence; prepn. of fusion protein contg.
 Mycobacterium tuberculosis heat shock protein HSP65 and T-cell
 epitopes and its use as vaccine for treatment of tuberculosis)

IT 1169721-44-1P
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (nucleotide sequence; prepn. of fusion protein contg.
 Mycobacterium tuberculosis heat shock protein HSP65 and T-cell
 epitopes and its use as vaccine for treatment of tuberculosis)

IT 1169721-54-3 1169721-55-4 1169721-56-5 1169721-57-6 1169721-58-7
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES
(Uses)
 (nucleotide sequence; prepn. of fusion protein contg.)

Mycobacterium tuberculosis heat shock protein HSP65 and T-cell epitopes and its use as vaccine for treatment of tuberculosis)

L8 ANSWER 3 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2008:1080164 CAPLUS <<LOGINID::20090924>>

DN 149:347463

TI Preparation of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy

IN Liu, Jingjing; Xie, Yanfei; Lu, Yong; Wu, Guojun; Lin, Ming; Fan, Hao; Wu, Jie; Cao, Rongyue

PA China Pharmaceutical University, Peop. Rep. China

SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 22pp.

CODEN: CNXXEV

DT Patent

LA Chinese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CN 101254301	A	20080903	CN 2007-10133868	20071024
PRAI	CN 2007-10133868		20071024		
AB The invention relates to application of ***HSP*** ***65*** recombinant protein from ***Mycobacterium*** bovine M17705 in prepg. antitumor drugs for treating mammary cancer, liver cancer, prostate caner, lung cancer and melanoma. The recombinant ***HSP*** ***65*** protein is prepd. by extg. genomic DNA from BCG vaccine, amplifying ***HSP*** ***65*** gene by PCR, inserting ***HSP*** ***65*** gene into plasmid vector pET-28a to obtain recombinant plasmid pET28a- ***HSP*** ***65***, transforming into E. coli to obtain engineered E. coli BL21/pET-28a- ***HSP*** ***65***, fermenting at 36-38.degree.C and pH 6.8-7.2, centrifugating fermn. broth, pptg. with ammonium sulfate, purifying by ion exchange chromatog. to obtain recombinant ***HSP*** ***65***, detecting by SDS-PAGE. The invention also provides nucleotide sequences of ***primers*** and PCR system for amplifying ***HSP*** ***65*** gene. The recombinant ***HSP*** ***65*** protein can significantly inhibit intratumor and peritumoral angiogenesis, inhibit metastasis of tumor cells, prevent and treat tumor formation.					
TI Preparation of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy					
AB The invention relates to application of ***HSP*** ***65*** recombinant protein from ***Mycobacterium*** bovine M17705 in prepg. antitumor drugs for treating mammary cancer, liver cancer, prostate caner, lung cancer and melanoma. The recombinant ***HSP*** ***65*** protein is prepd. by extg. genomic DNA from BCG vaccine, amplifying ***HSP*** ***65*** gene by PCR, inserting ***HSP*** ***65*** gene into plasmid vector pET-28a to obtain recombinant plasmid pET28a- ***HSP*** ***65***, transforming into E. coli to obtain engineered E. coli BL21/pET-28a- ***HSP*** ***65***, fermenting at 36-38.degree.C and pH 6.8-7.2, centrifugating fermn. broth, pptg. with ammonium sulfate, purifying by ion exchange chromatog. to obtain recombinant ***HSP*** ***65***, detecting by SDS-PAGE. The invention also provides nucleotide sequences of ***primers*** and PCR system for amplifying ***HSP*** ***65*** gene. The recombinant ***HSP*** ***65*** protein can significantly inhibit intratumor and peritumoral angiogenesis, inhibit metastasis of tumor cells, prevent and treat tumor formation.					
ST	recombinant heat shock protein ***Mycobacterium*** HSP65 antitumor				

agent

IT Plasmid vectors
(BL21/pET-28a-HSP65; prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Extraction
(DNA; prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Heat-shock proteins
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(***HSP*** ***65*** ; prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(Hsp65; prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Angiogenesis
(neovascularization; prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Plasmid vectors
(pET-28a; prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Plasmid vectors
(pET28a-HSP65; prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Angiogenesis inhibitors

Antitumor agents

Centrifugation

DNA sequences

Fermentation

Gel electrophoresis

Human

Ion exchange liquid chromatography

Liver, neoplasm

Lung, neoplasm

Mammary gland, neoplasm

Melanoma

Metastasis

Molecular cloning
Mycobacterium BCG
Mycobacterium bovis

Polymerase chain reaction

Precipitation (chemical)

Prostate gland, neoplasm

Salting-out
(prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Fusion proteins (chimeric proteins)

RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT Deoxyribonucleoside triphosphates
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT 1056089-38-3 1056089-39-4
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT 140002-36-4, GenBank M17705
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT 9012-90-2, PFU DNA polymerase 81295-22-9 92228-44-9
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

IT 100-37-8, DEAE 7783-20-2, Ammonium sulfate, uses
RL: NUU (Other use, unclassified); USES (Uses)
(prepn. of ***Mycobacterium*** bovis HSP65 recombinant protein and uses in tumor therapy)

L8 ANSWER 4 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2009:14410 CAPLUS <<LOGINID::20090924>>
DN 150:255335
TI rpoB sequence-based identification of ***Mycobacterium*** avium complex species
AU Ben Salah, Iskandar; Adekambi, Toidi; Raoult, Didier; Drancourt, Michel
CS Unite de Recherche sur les Maladies Infectieuses et Tropicales Emergentes, UMR, CNRS-IRD 6236, IFR 48 Faculte de Medecine, Universite de la Mediterranee, Marseille, Fr.
SO Microbiology (Reading, United Kingdom) (2008), 154(12), 3715-3723
CODEN: MROBEO; ISSN: 1350-0872
PB Society for General Microbiology
DT Journal
LA English
AB The ***Mycobacterium*** avium complex (MAC) comprises slowly growing ***mycobacteria*** responsible for opportunistic infections and zoonoses. The ability to speciate MAC isolates in the clin. microbiol. lab. is crit. for detg. the organism implicated in clin. disease and for epidemiol. investigation of the source of infection. Investigation of a 711 bp variable fragment of rpoB flanked by the Myco-F/Myco-R ***primers*** found a 0.7-5.1 % divergence among MAC ref. strains, with ***Mycobacterium*** chimaera and ***Mycobacterium*** intracellulare being the most closely related. Using a 0.7 % divergence cut-off, 83 % of 100 clin. isolates, which had been previously identified by phenotypic characteristics and 16S-23S rDNA intergenic spacer (ITS) probing, were identified as M. avium, 8 % as M. intracellulare and 2 % as M. chimaera.

The uniqueness of seven isolates, exhibiting <99.3 % rpoB sequence similarity with MAC ref. strains, was confirmed by 16S rDNA, ITS and hsp65 sequencing and phylogenetic analyses. Partial rpoB gene sequencing using the Myco-F/Myco-R ***primers*** permits one-step identification of MAC isolates at the species level and the detection of potentially novel MAC species.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI rpoB sequence-based identification of ***Mycobacterium*** avium complex species

AB The ***Mycobacterium*** avium complex (MAC) comprises slowly growing ***mycobacteria*** responsible for opportunistic infections and zoonoses. The ability to speciate MAC isolates in the clin. microbiol. lab. is crit. for. . . epidemiol. investigation of the source of infection. Investigation of a 711 bp variable fragment of rpoB flanked by the Myco-F/Myco-R ***primers*** found a 0.7-5.1 % divergence among MAC ref. strains, with ***Mycobacterium*** chimaera and ***Mycobacterium*** intracellulare being the most closely related. Using a 0.7 % divergence cut-off, 83 % of 100 clin. isolates, which had. . . strains, was confirmed by 16S rDNA, ITS and hsp65 sequencing and phylogenetic analyses. Partial rpoB gene sequencing using the Myco-F/Myco-R ***primers*** permits one-step identification of MAC isolates at the species level and the detection of potentially novel MAC species.

ST rpoB sequence ***Mycobacterium*** avium complex species identification

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** ***65*** ; rpoB sequence-based identification of ***Mycobacterium*** avium complex species)

IT Genetic element
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(IGS (intergenic spacer), 16S-23S rRNA genes; rpoB sequence-based identification of ***Mycobacterium*** avium complex species)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(RpoB; rpoB sequence-based identification of ***Mycobacterium*** avium complex species)

IT ***Mycobacterium*** avium
(complex; rpoB sequence-based identification of ***Mycobacterium*** avium complex species)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(hsp65; rpoB sequence-based identification of ***Mycobacterium*** avium complex species)

IT Human
(idolates; rpoB sequence-based identification of ***Mycobacterium*** avium complex species)

IT DNA sequence analysis
(in diagnosis; rpoB sequence-based identification of ***Mycobacterium*** avium complex species)

IT Epidemiology
(mol., identification of ***Mycobacterium*** avium complex for;

rpoB sequence-based identification of ***Mycobacterium*** avium
 complex species)

IT Evolution
 (mol.; rpoB sequence-based identification of ***Mycobacterium***
 avium complex species)

IT Protein sequences
 (of RpoB and HSP65 proteins; rpoB sequence-based identification of
 Mycobacterium avium complex species)

IT Databases
 (of rpoB partial sequences for ***Mycobacterium*** avium complex,
 contraction; rpoB sequence-based identification of
 Mycobacterium avium complex species)

IT DNA sequences
 Mycobacterium avium
 Mycobacterium avium hominissuis
 Mycobacterium avium paratuberculosis
 Mycobacterium avium silvaticum
 Mycobacterium chimerae
 Mycobacterium colombiense
 Mycobacterium intracellulare

Species differences
 (rpoB sequence-based identification of ***Mycobacterium*** avium
 complex species)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (rpoB sequence-based identification of ***Mycobacterium*** avium
 complex species)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (rpoB; rpoB sequence-based identification of ***Mycobacterium***
 avium complex species)

IT	1116734-54-3	1116734-56-5	1116734-58-7	1116734-60-1	1116734-67-8
	1116734-69-0	1116734-71-4	1116734-73-6	1116734-75-8	1116734-77-0
	1116738-60-3	1116738-62-5	1116738-64-7	1116738-66-9	1116738-68-1
	1116738-70-5	1116738-76-1	1116738-78-3	1116738-80-7	1116738-82-9

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; rpoB sequence-based identification of
 Mycobacterium avium complex species)

IT	1116734-47-4	1116734-48-5	1116734-49-6	1116734-50-9	1116734-51-0
	1116734-52-1	1116734-53-2	1116734-55-4	1116734-57-6	1116734-59-8
	1116734-61-2	1116734-62-3	1116734-63-4	1116734-64-5	1116734-65-6
	1116734-66-7	1116734-68-9	1116734-70-3	1116734-72-5	1116734-74-7
	1116734-76-9	1116734-88-3	1116734-89-4	1116734-90-7	1116734-91-8
	1116734-92-9	1116734-93-0	1116738-59-0	1116738-61-4	1116738-63-6
	1116738-65-8	1116738-67-0	1116738-69-2	1116738-71-6	1116738-72-7
	1116738-73-8	1116738-74-9	1116738-75-0	1116738-77-2	1116738-79-4
	1116738-81-8	1116740-95-4	1116740-96-5	1116740-97-6	1116740-98-7
	1116740-99-8				

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide sequence; rpoB sequence-based identification of
 Mycobacterium avium complex species)

IT 1121532-56-6
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);

ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** Myco-F; rpoB sequence-based identification of
Mycobacterium avium complex species)

IT 1121532-57-7

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** Myco-R; rpoB sequence-based identification of
Mycobacterium avium complex species)

L8 ANSWER 5 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:1141461 CAPLUS <>LOGINID::20090924>>
DN 149:549371
TI Identification of individual DNA molecule of ***Mycobacterium***
tuberculosis by nested PCR-RFLP and capillary electrophoresis
AU Chang, Po-Ling; Hsieh, Wen-Shyang; Chiang, Chia-Lien; Yen-Liberman,
Belinda; Procop, Gary W.; Chang, Huan-Tsung; Ho, Hsin-Tsung
CS Department of Chemistry, National Taiwan University, Taipei, Taiwan
SO Talanta (2008), 77(1), 182-188
CODEN: TLNTA2; ISSN: 0039-9140
PB Elsevier B.V.
DT Journal
LA English
AB The improvement of sensitivity and differentiation in rapidly identifying
a small amt. of ***mycobacteria*** in sputum has significant
implications for reducing tuberculosis transmission. We previously
applied the conventional PCR and capillary electrophoresis (CE) to
establish the restriction fragment length polymorphism (RFLP) pattern of
mycobacterial 65-kDa heat shock protein (hsp65) gene from colony
specimens. However, the previous anal. did not provide enough sensitivity
for sputum specimens in which the limitation of anal. might be hindered by
PCR inhibitors and ***primer*** -dimers formation during amplification.
In the current study, nested PCR (nPCR) had been redesigned for PCR-RFLP
anal. (PRA) of ***mycobacterial*** hsp65 gene using CE. The results
show both ***Mycobacterium*** tuberculosis complex and
mycobacteria other than tuberculosis could be identified in the
presence of PCR inhibitors. The interference due to ***primer***
-dimers was also minimized. Based on the Poisson distribution, the
repeatability of single DNA mol. detection was greatly affected by
sampling probability and might be improved significantly by increasing the
sample loading. The PRA using nPCR and CE is not only able to detect the
individual ***mycobacterial*** DNA mol. but also potentially
differentiate the species.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Identification of individual DNA molecule of ***Mycobacterium***
tuberculosis by nested PCR-RFLP and capillary electrophoresis
AB The improvement of sensitivity and differentiation in rapidly identifying
a small amt. of ***mycobacteria*** in sputum has significant
implications for reducing tuberculosis transmission. We previously
applied the conventional PCR and capillary electrophoresis (CE) to
establish the restriction fragment length polymorphism (RFLP) pattern of
mycobacterial 65-kDa heat shock protein (hsp65) gene from colony
specimens. However, the previous anal. did not provide enough sensitivity
for sputum specimens in which the limitation of anal. might be hindered by
PCR inhibitors and ***primer*** -dimers formation during amplification.
In the current study, nested PCR (nPCR) had been redesigned for PCR-RFLP

anal. (PRA) of ***mycobacterial*** hsp65 gene using CE. The results show both ***Mycobacterium*** tuberculosis complex and ***mycobacteria*** other than tuberculosis could be identified in the presence of PCR inhibitors. The interference due to ***primer***-dimers was also minimized. Based on the Poisson distribution, the repeatability of single DNA mol. detection was greatly affected by sampling. . . significantly by increasing the sample loading. The PRA using nPCR and CE is not only able to detect the individual ***mycobacterial*** DNA mol. but also potentially differentiate the species.

ST ***Mycobacterium*** single mol detection nested PCR RFLP capillary electrophoresis; hsp65 gene detection ***Mycobacterium*** tuberculosis diagnosis PCR capillary electrophoresis

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (***HSP*** ***65*** , gene, detection; identification of individual DNA mol. of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis)

IT Sputum
 (***Mycobacterium*** detection; identification of individual DNA mol. of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis)

IT Gene, microbial
 RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (hsp65; identification of individual DNA mol. of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis)

IT Capillary electrophoresis
 Mycobacterium celatum
 Mycobacterium heckeshornense
 Mycobacterium tuberculosis
 Restriction fragment length polymorphism
 Single molecule detection
 Tuberculosis
 (identification of individual DNA mol. of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis)

IT Diagnosis
 (mol.; identification of individual DNA mol. of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis)

IT Polymerase chain reaction
 (nested; identification of individual DNA mol. of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis)

IT ***Mycobacterium***
 (species identification; identification of individual DNA mol. of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis)

IT 1082081-74-0 1082081-75-1 1082081-76-2 1082081-77-3 1082081-78-4
 1082081-79-5
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR ***primer*** ; identification of individual DNA mol. of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis)

IT 81295-18-3
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (identification of individual DNA mol. of ***Mycobacterium***)

tuberculosis by nested PCR-RFLP and capillary electrophoresis)

L8 ANSWER 6 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:962412 CAPLUS <>LOGINID::20090924>>
DN 150:275953
TI A single-step sequencing method for the identification of
Mycobacterium tuberculosis complex species
AU Djelouadji, Zoheira; Raoult, Didier; Daffe, Mamadou; Drancourt, Michel
CS Unite des Rickettsies CNRS UMR6020, IFR 48, Faculte de Medecine,
Universite de la Mediterranee, Marseille, Fr.
SO PLoS Neglected Tropical Diseases (2008), 2(6), No pp. given
CODEN: PNTDAM; ISSN: 1935-2735
URL: <http://www.plosntds.org/article/info%3Adoi%2F10.1371%2Fjournal.pntd.000253>
PB Public Library of Science
DT Journal; (online computer file)
LA English
AB The ***Mycobacterium*** tuberculosis complex (MTC) comprises closely related species responsible for strictly human and zoonotic tuberculosis. Accurate species detn. is useful for the identification of outbreaks and epidemiol. links. ***Mycobacterium*** africanum and ***Mycobacterium*** canettii are typically restricted to Africa and M. bovis is a re-emerging pathogen. Identification of these species is difficult and expensive. The Exact Tandem Repeat D (ETR-D; alias ***Mycobacterial*** Interspersed Repetitive Unit 4) was sequenced in
MTC species type strains and 110 clin. isolates, in parallel to ref. polyphasic identification based on phenotype profiling and sequencing of pncA, oxyR, hsp65, gyrB genes and the major polymorphism tandem repeat. Inclusion of M. tuberculosis isolates in the expanding, antibiotic-resistant Beijing clone was detd. by Rv0927c gene sequencing. The ETR-D (780-bp) sequence unambiguously identified MTC species type strain except M. pinnipedii and M. microti due to six single nucleotide polymorphisms, variable nos. (1-7 copies) of the tandem repeat and two deletions/insertions. The ETR-D sequencing agreed with phenotypic identification in 107/110 clin. isolates and with ref. polyphasic mol. identification in all isolates, comprising 98 M. tuberculosis, 5 M. bovis BCG type, 5 M. canettii, and 2 M. africanum. For M. tuberculosis isolates, the ETR-D sequence was not significantly assocd. with the Beijing clone. ETR-D sequencing allowed accurate, single-step identification of the MTC at the species level. It circumvented the current expensive, time-consuming polyphasic approach. It could be used to depict epidemiol. of zoonotic and human tuberculosis, esp. in African countries where several MTC species are emerging.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 70 THERE ARE 70 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI A single-step sequencing method for the identification of
Mycobacterium tuberculosis complex species
AB The ***Mycobacterium*** tuberculosis complex (MTC) comprises closely related species responsible for strictly human and zoonotic tuberculosis. Accurate species detn. is useful for the identification of outbreaks and epidemiol. links. ***Mycobacterium*** africanum and ***Mycobacterium*** canettii are typically restricted to Africa and M. bovis is a re-emerging pathogen. Identification of these species is difficult and expensive. The Exact Tandem Repeat D (ETR-D; alias

Mycobacterial Interspersed Repetitive Unit 4) was sequenced in MTC species type strains and 110 clin. isolates, in parallel to ref. polyphasic. . .

ST PCR exact tandem repeat D ***Mycobacterium*** species identification; DNA sequence Senx3 Regx3 intergenic spacer ETRD repeat ***Mycobacterium*** ; sequence DNA gene oxyR hsp65 ***Mycobacterium*** ; ***primer*** PCR DNA repeat ETRD ***Mycobacterium*** species identification

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT Cell morphology
Phenotypes
(ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and phenotypic characteristics)

IT ***Mycobacterium*** tuberculosis
Polymerase chain reaction
(ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** ***65*** ; partial DNA and amino acid sequences of novel oxyR, hsp65 and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

IT Genetic element
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(IGS (intergenic spacer), ETR-D repeat located in Senx3-Regx3 spacer region; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Genetic polymorphism
(INDEL; ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and phenotypic characteristics)

IT Transcription factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(OxyR; partial DNA and amino acid sequences of novel oxyR, hsp65 and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Regx3, Senx3-Regx3 spacer region; partial DNA and amino acid sequences

of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Senx3, Senx3-Regx3 spacer region; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene Regx3, sensory transduction protein, sequence homolog; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene mptR; partial DNA and amino acid sequences of novel oxyR, hsp65 and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gyrB; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, hsp65, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hsp65; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, hsp65, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Diagnosis
(mol.; ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and phenotypic characteristics)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(mptR; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, hsp65, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(oxyR; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, hsp65, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT DNA sequences
Mycobacterium BCG
Mycobacterium africanum
Mycobacterium bovis

Mycobacterium canettii
 Mycobacterium caprae
 Mycobacterium microti
 Mycobacterium pinnipedii

Protein sequences
 (partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Single nucleotide polymorphism
 (partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, hsp65, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (pncA; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, hsp65, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT DNA
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** ; ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT Repetitive DNA
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (tandem, exact D, ETR-D in Senx3-Regx3 intergenic spacer; ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT Repetitive DNA
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (tandem; ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT 1124387-63-8 1124387-64-9
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (ETR-D-specific ***primer*** ; ETR-D sequencing for single-step identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT 1123333-08-3 1123333-09-4 1123333-11-8 1123333-12-9 1123333-14-1
 1123333-15-2 1123333-17-4 1123333-18-5 1123333-20-9 1123333-21-0
 1123333-23-2 1123333-24-3 1123333-26-5 1123333-27-6
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3

intergenic spacer that contains the ETR-D repeat)
 IT 1088759-76-5 1088759-78-7 1088759-80-1
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; partial DNA and amino acid sequences of novel
 oxyR, hsp65 and mptR genes found in ***Mycobacterium*** canettii
 and M. africanum)
 IT 420839-67-4
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (gene Senx3, sequence homolog; partial DNA and amino acid sequences of
 Mycobacterium genes Senx3 and Regx3, including the Senx3-Regx3
 intergenic spacer that contains the ETR-D repeat)
 IT 1123333-07-2 1123333-10-7 1123333-13-0 1123333-16-3 1123333-19-6
 1123333-22-1 1123333-25-4
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic
 use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
 USES (Uses)
 (nucleotide sequence; partial DNA and amino acid sequences of
 Mycobacterium genes Senx3 and Regx3, including the Senx3-Regx3
 intergenic spacer that contains the ETR-D repeat)
 IT 1088759-75-4 1088759-77-6 1088759-79-8
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide sequence; partial DNA and amino acid sequences of novel
 oxyR, hsp65 and mptR genes found in ***Mycobacterium*** canettii
 and M. africanum)

L8 ANSWER 7 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2007:1057364 CAPLUS <>LOGINID::20090924>>
 DN 147:337125
 TI Method for differentiating or identifying ***Mycobacterium***
 tuberculosis and non-tuberculous ***mycobacteria*** using hsp65
 signature nucleotide sequence
 IN Kim, Bum Joon; Kim, Hyun Joo; Park, Hae Joon
 PA Seoul National University Industry Foundation, S. Korea
 SO Repub. Korea, No pp. given
 CODEN: KRXXFC
 DT Patent
 LA Korean
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 692484	B1	20070313	KR 2005-104871	20051103
PRAI	KR 2005-104871		20051103		
AB	A method for identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** is provided to conveniently and accurately differentiate ***Mycobacterial*** species by using each 8 signature nucleotide sequences capable of characterizing ***Mycobacterium*** tuberculosis group and non-tuberculous ***mycobacteria*** group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the group consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(HSP65) consisting of total 1623bp of ***Mycobacterial*** species using a ***primer*** specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the				

bases above to identify non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis, where the non-tuberculous ***mycobacteria*** is 228th base of C, 243th base of C, 543th base of C,
C,
600th base of C or T, 705th base of G or 718-720th bases of CAG, and the ***Mycobacterium*** tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base of C or 718-720th bases of GGA. The nucleotide sequence of ***primer*** pair for producing PCR amplification product specific to the non-tuberculous ***mycobacteria*** is described. The differentiation kit for non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis comprises a ***primer*** pairs, and the sequences of the ***primers*** have been presented.

TI Method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using hsp65 signature nucleotide sequence

AB A method for identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** is provided to conveniently and accurately differentiate ***Mycobacterial*** species by using each 8 signature nucleotide sequences capable of characterizing ***Mycobacterium*** tuberculosis group and non-tuberculous ***mycobacteria*** group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the . . 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(HSP65) consisting of total 1623bp of ***Mycobacterial*** species using a ***primer*** specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the bases above to identify non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis, where the non-tuberculous ***mycobacteria*** is 228th base of C, 243th base of C, 543th base of C, 600th base of C or T, 705th base of G or 718-720th bases of CAG, and the ***Mycobacterium*** tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base of C or 718-720th bases of GGA. The nucleotide sequence of ***primer*** pair for producing PCR amplification product specific to the non-tuberculous ***mycobacteria*** is described. The differentiation kit for non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis comprises a ***primer*** pairs, and the sequences of the ***primers*** have been presented.

ST ***Mycobacterium*** tuberculosis nontuberculous genotyping PCR Hsp65 gene

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** ; method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using hsp65 signature nucleotide sequence)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(hsp65; method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using hsp65 signature nucleotide sequence)

IT Genotypes
Genotyping (method)
Mycobacterium
Mycobacterium tuberculosis

Polymerase chain reaction

Tuberculosis

(method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using hsp65 signature nucleotide sequence)

IT ***Primers*** (nucleic acid)

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses) (method for differentiating or identifying ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using hsp65 signature nucleotide sequence)

L8 ANSWER 8 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2007:329817 CAPLUS <<LOGINID::20090924>>

DN 146:352579

TI Detection of bacteria from the ***Mycobacterium*** tuberculosis complex using real-time PCR

IN Chomarat, Monique; Breysse, Franck

PA Hospices Civils de Lyon, Fr.; Universite Claude Bernard

SO Fr. Demande, 40pp.

CODEN: FRXXBL

DT Patent

LA French

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	FR 2890978	A1	20070323	FR 2005-9587	20050920
	WO 2007034118	A1	20070329	WO 2006-FR50916	20060920
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW				
	RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				

PRAI FR 2005-9587 A 20050920

AB This invention relates to detection of microbes from the ***Mycobacterium*** tuberculosis complex (Mtbc) from biol. samples, using real-time PCR. The microbial gene hsp65 was amplified and detected by fluorescence assoccd. with real-time PCR amplification using provided ***primers*** and fluorescently-labeled probes (fluorescein, LC Red640, LC Red670 or LC Red705). An internal control construct comprising lambda phage DNA flanked on each end by short Mtbc-specific gene hsp65 sequences was cloned into plasmid DNA and used to det. lower limits of PCR detection. Evaluation of real-time PCR melting curves enabled detection of Mtbc-specific bacteria.

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Detection of bacteria from the ***Mycobacterium*** tuberculosis complex using real-time PCR

AB This invention relates to detection of microbes from the ***Mycobacterium*** tuberculosis complex (Mtbc) from biol. samples,

using real-time PCR. The microbial gene hsp65 was amplified and detected by fluorescence assocd. with real-time PCR amplification using provided ***primers*** and fluorescently-labeled probes (fluorescein, LC Red640, LC Red670 or LC Red705). An internal control construct comprising lambda phage DNA flanked. . .

ST ***Mycobacteria*** tuberculosis complex detection real time PCR; real time PCR ***primer*** probe sequence ***Mycobacterium*** detection; bacteriophage lambda DNA sequence PCR internal control Coliphage .lambda.

IT (DNA; detection of ***Mycobacterium*** tuberculosis complex bacteria using real-time PCR)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (FRET, anchor, hybridization; detection of ***Mycobacterium*** tuberculosis complex bacteria using real-time PCR)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (***HSP*** ***65*** , gene hsp65; detection of
 Mycobacterium tuberculosis complex bacteria using real-time PCR)

IT ***Mycobacterium*** frederiksbergense
 (I; detection of ***Mycobacterium*** tuberculosis complex bacteria using real-time PCR)

IT ***Mycobacterium*** tuberculosis
 (complex; detection of ***Mycobacterium*** tuberculosis complex bacteria using real-time PCR)

IT Corynebacterium argentoratense
Corynebacterium auriscanis
Corynebacterium confusum
Corynebacterium diphtheriae
Corynebacterium durum
Corynebacterium felinum
Corynebacterium kroppenstedtii
Corynebacterium macginleyi
Corynebacterium mastitidis
Corynebacterium matruchotii
Corynebacterium mycetoides
Corynebacterium phocae
Corynebacterium pilosum
Corynebacterium simulans
Corynebacterium striatum
Corynebacterium vitaeruminis
Fluorescence
Fluorescent dyes
Liquidus
Melting point

Mycobacterium	BCG
Mycobacterium	abscessus
Mycobacterium	africanum
Mycobacterium	aichiense
Mycobacterium	alvei
Mycobacterium	asiaticum
Mycobacterium	austroafricanum
Mycobacterium	avium avium
Mycobacterium	avium silvaticum

	Mycobacterium	botniense
	Mycobacterium	bovis
	Mycobacterium	branderi
	Mycobacterium	brumae
	Mycobacterium	celatum
	Mycobacterium	chelonae
	Mycobacterium	chitae
	Mycobacterium	chlorophenolicum
	Mycobacterium	confluentis
	Mycobacterium	cookii
	Mycobacterium	diernhoferi
	Mycobacterium	doricum
	Mycobacterium	duvalii
	Mycobacterium	fallax
	Mycobacterium	farcinogenes
	Mycobacterium	flavescens
	Mycobacterium	fortuitum fortuitum
	Mycobacterium	gadium
	Mycobacterium	gastri
	Mycobacterium	genavense
	Mycobacterium	gilvum
	Mycobacterium	gordonae
	Mycobacterium	haemophilum
	Mycobacterium	hassiacum
	Mycobacterium	heckeshornense
	Mycobacterium	hiberniae
	Mycobacterium	hodleri
	Mycobacterium	interjectum
	Mycobacterium	leprae
	Mycobacterium	microti
	Mycobacterium	nonchromogenicum
	Mycobacterium	porcinum
	Mycobacterium	shimoidei
	Mycobacterium	triviale
	Mycobacterium	tuberculosis caprae
	Mycobacterium	tuberculosis tuberculosis
	Mycobacterium	wolinskyi
	Mycobacterium	xenopi
	Nocardia asteroides	
	Nocardia brasiliensis	
	Nocardia farcinica	
	Nocardia otitidiscaziarum	
	Nucleic acid hybridization	
	Propionibacterium acnes	
	Propionibacterium granulosum	
	Test kits	
	(detection of ***Mycobacterium*** tuberculosis complex bacteria using real-time PCR)	
IT	***Primers*** (nucleic acid)	
	RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)	
	(detection of ***Mycobacterium*** tuberculosis complex bacteria using real-time PCR)	
IT	Gene, microbial	
	RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL	

(Biological study); USES (Uses)
(for .lambda. phage, internal control DNA, detection of; detection of
Mycobacterium tuberculosis complex bacteria using real-time
PCR)

IT Gene, microbial
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(hsp65, detection of; detection of ***Mycobacterium*** tuberculosis
complex bacteria using real-time PCR)

IT Polymerase chain reaction
(real-time, Light Cycler; detection of ***Mycobacterium***
tuberculosis complex bacteria using real-time PCR)

IT DNA sequences
(.lambda. phage DNA and gene hsp65, from M. tuberculosis; detection of
Mycobacterium tuberculosis complex bacteria using real-time
PCR)

IT 930118-32-4D, LightCycler Red 670, 5'-conjugation of probes
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(LC Red 670; detection of ***Mycobacterium*** tuberculosis complex
bacteria using real-time PCR)

IT 2321-07-5D, Fluorescein, 3'-conjugation of probes 245670-26-2D, LC Red
640, 5'-conjugation of probes 251949-03-8D, LC-RED 705, 5'-conjugation
of probes
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(detection of ***Mycobacterium*** tuberculosis complex bacteria
using real-time PCR)

IT 930128-82-8
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(nucleotide sequence; detection of ***Mycobacterium*** tuberculosis
complex bacteria using real-time PCR)

IT 930128-73-7 930128-74-8 930128-81-7
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(***primer*** sequence; detection of ***Mycobacterium***
tuberculosis complex bacteria using real-time PCR)

IT 930128-75-9D, 3'-conjugation with fluorescein 930128-76-0D,
5'-conjugation with LC Red640 930128-77-1D, 3'-conjugation with
fluorescein 930128-78-2D, 5'-conjugation with LC Red670 930128-79-3D,
3'-conjugation with fluorescein 930128-80-6D, 5'-conjugation with LC
Red705
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(probe sequence; detection of ***Mycobacterium*** tuberculosis
complex bacteria using real-time PCR)

IT 930129-12-7 930129-13-8
RL: PRP (Properties)
(unclaimed nucleotide sequence; detection of bacteria from the
Mycobacterium tuberculosis complex using real-time PCR)

L8 ANSWER 9 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:1153666 CAPLUS <<LOGINID::20090924>>
DN 148:300509
TI ***Mycobacterium*** species identification - a new approach via dnaJ
gene sequencing
AU Yamada-Noda, Makiko; Ohkusu, Kiyofumi; Hata, Hiroyuki; Shah, Mohammad
Monir; Nhung, Pham Hong; Sun, Xiao Song; Hayashi, Masahiro; Ezaki,
Takayuki
CS Department of Microbiology, Regeneration and Advanced Medical Science,
Gifu University Graduate School of Medicine, 1-1 Yanagido, Gifu, 501-1194,
Japan
SO Systematic and Applied Microbiology (2007), 30(6), 453-462
CODEN: SAMIDF; ISSN: 0723-2020
PB Elsevier GmbH
DT Journal
LA English
AB The availability of the dnaJ1 gene for identifying ***Mycobacterium***
species was examd. by analyzing the complete dnaJ1 sequences (approx. 1200
bp) of 56 species (54 of them were type strains) and comparing sequence
homologies with those of the 16S rRNA gene and other housekeeping genes
(rpoB, hsp65). Among the 56 ***Mycobacterium*** species, the mean
sequence similarity of the dnaJ1 gene (80.4%) was significantly less than
that of the 16S rRNA, rpoB and hsp65 genes (96.6%, 91.3% and 91.1%,
resp.), indicating a high discriminatory power of the dnaJ1 gene.
Seventy-one clin. isolates were correctly clustered to the corresponding
type strains, showing isolates belonging to the same species. In order to
propose a method for strain identification, we identified an area with a
high degree of polymorphism, bordered by conserved sequences, that can be
used as universal ***primers*** for PCR amplification and sequencing.
The sequence of this fragment (approx. 350 bp) allows accurate species
identification and may be used as a new tool for the identification of
Mycobacterium species.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI ***Mycobacterium*** species identification - a new approach via dnaJ
gene sequencing
AB The availability of the dnaJ1 gene for identifying ***Mycobacterium***
species was examd. by analyzing the complete dnaJ1 sequences (approx. 1200
bp) of 56 species (54 of them were type. . . and comparing sequence
homologies with those of the 16S rRNA gene and other housekeeping genes
(rpoB, hsp65). Among the 56 ***Mycobacterium*** species, the mean
sequence similarity of the dnaJ1 gene (80.4%) was significantly less than
that of the 16S rRNA, rpoB. . . we identified an area with a high
degree of polymorphism, bordered by conserved sequences, that can be used
as universal ***primers*** for PCR amplification and sequencing. The
sequence of this fragment (approx. 350 bp) allows accurate species
identification and may be used as a new tool for the identification of
Mycobacterium species.
ST ***Mycobacterium*** identification taxonomy dnaJ gene sequence; rDNA
sequence ***Mycobacterium*** Nocardia; heat shock protein HSP65 gene
sequence Nocardia ***Mycobacterium***
IT rRNA
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(16 S, rDNA sequences; ***Mycobacterium*** species identification

by dnaJ gene sequencing)

IT Molecular chaperones
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(DnaJ, gene dnaJ1; ***Mycobacterium*** species identification by dnaJ gene sequencing)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** ***65*** , gene Hsp65; ***Mycobacterium*** species identification by dnaJ gene sequencing)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Hsp65; ***Mycobacterium*** species identification by dnaJ gene sequencing)

IT Bacterial infection
DNA sequences
Genetic polymorphism
Human

Mycobacterium	abscessus
Mycobacterium	africanum
Mycobacterium	alvei
Mycobacterium	arupense
Mycobacterium	asiaticum
Mycobacterium	aubagnense
Mycobacterium	avium avium
Mycobacterium	avium silvaticum
Mycobacterium	bolletii
Mycobacterium	bovis
Mycobacterium	branderi
Mycobacterium	caprae
Mycobacterium	celatum
Mycobacterium	chelonae
Mycobacterium	chimerae
Mycobacterium	chitae
Mycobacterium	cookii
Mycobacterium	flavescens
Mycobacterium	fortuitum
Mycobacterium	gastri
Mycobacterium	genavense
Mycobacterium	gilvum
Mycobacterium	gordonae
Mycobacterium	haemophilum
Mycobacterium	hiberniae
Mycobacterium	houstonense
Mycobacterium	interjectum
Mycobacterium	intermedium
Mycobacterium	intracellulare
Mycobacterium	kansasii
Mycobacterium	kumamotoense
Mycobacterium	lentiflavum
Mycobacterium	leprae
Mycobacterium	malmoense
Mycobacterium	marinum
Mycobacterium	microti
Mycobacterium	mucogenicum

Mycobacterium neworleansense
 Mycobacterium nonchromogenicum
 Mycobacterium parafortuitum
 Mycobacterium peregrinum
 Mycobacterium phlei
 Mycobacterium phocaicum
 Mycobacterium porcinum
 Mycobacterium scrofulaceum
 Mycobacterium senegalense
 Mycobacterium septicum
 Mycobacterium shimoidei
 Mycobacterium simiae
 Mycobacterium smegmatis
 Mycobacterium szulgai
 Mycobacterium terrae
 Mycobacterium triviale
 Mycobacterium tuberculosis
 Mycobacterium ulcerans
 Mycobacterium vaccae
 Mycobacterium xenopi

 Nocardia nova
 Polymerase chain reaction
 Protein sequences
 Taxonomy
 (***Mycobacterium*** species identification by dnaJ gene sequencing)
 IT Gene, microbial
 RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (dnaJ1; ***Mycobacterium*** species identification by dnaJ gene sequencing)
 IT Evolution
 (mol., sequence phylogeny; ***Mycobacterium*** species identification by dnaJ gene sequencing)
 IT Diagnosis
 (mol.; ***Mycobacterium*** species identification by dnaJ gene sequencing)
 IT Gene, microbial
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (rpoB; ***Mycobacterium*** species identification by dnaJ gene sequencing)
 IT 1009651-94-8 1009651-95-9
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR ***primer*** ; ***Mycobacterium*** species identification by dnaJ gene sequencing)
 IT 1007158-10-2 1007158-12-4 1007158-14-6 1007158-16-8 1007158-18-0
 1007158-20-4 1007158-22-6 1007158-24-8 1007158-26-0 1007158-28-2
 1007158-30-6 1007158-32-8 1007158-34-0 1007158-36-2 1007158-38-4
 1007158-40-8 1007158-42-0 1007158-44-2 1007158-46-4 1007158-48-6
 1007158-50-0 1007158-52-2 1007158-54-4 1007158-56-6 1007158-58-8
 1007158-60-2 1007158-62-4 1007158-64-6 1007158-66-8 1007158-68-0
 1007158-70-4 1007158-72-6 1007158-74-8 1007158-76-0 1007158-78-2
 1007158-80-6 1007158-82-8 1007158-84-0 1007158-86-2 1007158-88-4
 1007158-90-8 1007158-92-0 1007158-94-2 1007158-96-4 1007158-98-6

1007159-00-3 1007159-02-5 1007159-04-7 1007159-06-9 1007159-08-1
 1007159-10-5 1007159-12-7 1007159-14-9 1007159-16-1 1007159-18-3
 1007159-20-7 1007159-22-9 1007159-27-4 1007159-29-6
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; ***Mycobacterium*** species identification by
 dnaJ gene sequencing)

IT 1007158-09-9 1007158-11-3 1007158-13-5 1007158-15-7 1007158-17-9
 1007158-19-1 1007158-21-5 1007158-23-7 1007158-25-9 1007158-27-1
 1007158-29-3 1007158-31-7 1007158-33-9 1007158-35-1 1007158-37-3
 1007158-39-5 1007158-41-9 1007158-43-1 1007158-45-3 1007158-47-5
 1007158-49-7 1007158-51-1 1007158-53-3, DNA (***Mycobacterium***
 leprae gene dnaJ1) 1007158-55-5 1007158-57-7 1007158-59-9
 1007158-61-3 1007158-63-5 1007158-65-7 1007158-67-9 1007158-69-1
 1007158-71-5 1007158-73-7 1007158-75-9 1007158-77-1 1007158-79-3
 1007158-81-7 1007158-83-9 1007158-85-1 1007158-87-3 1007158-89-5
 1007158-91-9 1007158-93-1 1007158-95-3 1007158-97-5 1007158-99-7
 1007159-01-4 1007159-03-6 1007159-05-8 1007159-07-0 1007159-09-2
 1007159-11-6 1007159-13-8 1007159-15-0 1007159-17-2 1007159-19-4
 1007159-21-8 1007159-23-0 1007159-24-1 1007159-25-2 1007159-26-3
 1007159-28-5
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide sequence; ***Mycobacterium*** species identification by
 dnaJ gene sequencing)

L8 ANSWER 10 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2007:736244 CAPLUS <>LOGINID::20090924>>
 DN 147:382888
 TI Detection of ***Mycobacterium*** species distribution in the sputum
 samples of tuberculosis patients by the PCR-RFLP method in Elazig province
 AU Agacayak, Ahmet; Bulut, Yasemin; Seyrek, Adnan
 CS Mikrobiyoloji ve Klinik Mikrobiyoloji Anabilim Dali, Firat Ueniversitesi
 Tip Fakultesi, Elazig, Turk.
 SO Mikrobiyoloji Bulteni (2007), 41(2), 203-209
 CODEN: MIBUBI; ISSN: 0374-9096
 PB Ankara Mikrobiyoloji Dernegi
 DT Journal
 LA Turkish
 AB The aim of this study was to detect the ***Mycobacterium*** species in
 the sputum samples collected from tuberculosis patients in Elazig province
 (located in Eastern Anatolia, Turkey), by PCR-RFLP (Polymerase Chain
 Reaction-Restriction Fragment Length Polymorphism) method. A total of 60
 samples from patients (32 male, 28 female) who were diagnosed as
 tuberculosis by culture positivity at Elazig Tuberculosis Control
 Dispensary, were included to the study. After DNA extn. and isolation
 from the samples, gene region encoding for 65 kDa protein of
 mycobacteria was amplified with specific ***primers*** (first
 step ***primers*** : TB1; 5'-GAG ATC GAC TGG AGG ATC C-3' and TB2;
 5'-AGC TGC AGC CCA MAAG GTG TT- 3', second step ***primers*** : TB1 and
 TB3; 5'-GTG TTG GAC TCC TCG ACG GT-3') by using semi-nested PCR method.
 According to hsp65 gene region amplification, 51 (85%) samples yielded
 pos. results, while nine (15%) samples could not be identified. Of 51
 samples, 44 (86.3%) were identified as M.tuberculosis complex, four (7.8%)
 were M.scrofulaceum, two (3.9%) were M.avium and one (1.9%) was
 M.intracellulare, in the restriction assay by HaeIII of the PCR products.
 In order to identify the species of M.tuberculosis complex, gyrB gene

region was amplified in those of 44 samples with specific ***primers*** (MTUB-f; 5'-TCG GAC GCG TAT GCG ATA TC-3' and MTUB-r; 5'-ACA TAC AGT TCG GAC TTG CG-3'), and the PCR products were restricted by RsaI and TaqI enzymes. In this assay, 34 (77.3%), eight (18.2%), one (2.3%) and one (2.3%) of the 44 M.tuberculosis complex samples were detected as M.tuberculosis, M.bovis, M.microti and M.africanum, resp. Our data indicated that at least seven different ***Mycobacterium*** species were the causative agents of tuberculosis in our region. As a result, researching for species distributions of ***mycobacteria*** in all of the parts of Turkey by mol. methods and clarifying their resistance patterns against antituberculous drugs are needed for the effective control of tuberculosis.

- TI Detection of ***Mycobacterium*** species distribution in the sputum samples of tuberculosis patients by the PCR-RFLP method in Elazig province
- AB The aim of this study was to detect the ***Mycobacterium*** species in the sputum samples collected from tuberculosis patients in Elazig province (located in Eastern Anatolia, Turkey), by PCR-RFLP (Polymerase. . . included to the study. After DNA extn. and isolation from the samples, gene region encoding for 65 kDa protein of ***mycobacteria*** was amplified with specific ***primers*** (first step ***primers*** : TB1; 5'-GAG ATC GAC TGG AGG ATC C-3' and TB2; 5'-AGC TGC AGC CCA MAAG GTG TT- 3', second step ***primers*** : TB1 and TB3; 5'-GTG TTG GAC TCC TCG ACG GT-3') by using semi-nested PCR method. According to hsp65 gene region. . . order to identify the species of M.tuberculosis complex, gyrB gene region was amplified in those of 44 samples with specific ***primers*** (MTUB-f; 5'-TCG GAC GCG TAT GCG ATA TC-3' and MTUB-r; 5'-ACA TAC AGT TCG GAC TTG CG-3'), and the PCR. . . M.tuberculosis complex samples were detected as M.tuberculosis, M.bovis, M.microti and M.africanum, resp. Our data indicated that at least seven different ***Mycobacterium*** species were the causative agents of tuberculosis in our region. As a result, researching for species distributions of ***mycobacteria*** in all of the parts of Turkey by mol. methods and clarifying their resistance patterns against antituberculous drugs are needed. . .
- ST ***Mycobacterium*** species sputum tuberculosis PCR RFLP Turkey
- IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study) (***HSP*** ***65*** ; detection of ***Mycobacterium*** species distribution in sputum samples of tuberculosis patients by PCR-RFLP method in Elazig province)
- IT Human
Mycobacterium
Restriction fragment length polymorphism
Sputum
Tuberculosis
(detection of ***Mycobacterium*** species distribution in sputum samples of tuberculosis patients by PCR-RFLP method in Elazig province)
- IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gyrB; detection of ***Mycobacterium*** species distribution in sputum samples of tuberculosis patients by PCR-RFLP method in Elazig province)
- IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(hsp65; detection of ***Mycobacterium*** species distribution in sputum samples of tuberculosis patients by PCR-RFLP method in Elazig province)

L8 ANSWER 11 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:365640 CAPLUS <>LOGINID::20090924>>
DN 147:2742
TI Detection of opportunistic infections by low-density microarrays. A diagnostic approach for granulomatous lymphadenitis
AU Odenthal, Margarete; Koenig, Sina; Farbrother, Patrick; Drebber, Uta; Bury, Yvonne; Dienes, Hans Peter; Eichinger, Ludwig
CS Institute for Pathology, University Clinic of Cologne, University of Cologne, Germany
SO Diagnostic Molecular Pathology (2007), 16(1), 18-26
CODEN: DMPAES; ISSN: 1052-9551
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB In mol. diagnosis of infectious diseases often more than 1 pathogen has to be considered. As a consequence, a series of labor-intensive and time-consuming polymerase chain reaction (PCR) approaches specific for different putative pathogens have to be carried out. To speed up diagnosis, we established a low-d. microarray for simultaneous detection of diverse putative pathogens causing a disease such as granulomatous lymphadenitis. Nucleic acids from formalin-fixed, paraffin-embedded tissues of 68 patients with lymphadenitis were used for mol. diagnosis of individual pathogens by either nested single-assay PCR or 1-step multiplex PCR in combination with low-d. microarray hybridization. Multiplex PCR amplicons hybridized to glass slides contg. probes from ***Mycobacterium*** spp., Yersinia spp., Bartonella henselae, Toxoplasma gondii, and other pathogens showed specific and reproducible signals on the array. Our results show that microarray technol. combined with multiplex PCR is a promising and time-saving tool in mol. pathol. of infectious diseases, allowing sensitive, simultaneous analyses of different pathogens.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB . . . or 1-step multiplex PCR in combination with low-d. microarray hybridization. Multiplex PCR amplicons hybridized to glass slides contg. probes from ***Mycobacterium*** spp., Yersinia spp., Bartonella henselae, Toxoplasma gondii, and other pathogens showed specific and reproducible signals on the array. Our results. . .
ST multiplex PCR microarray technol bacterial pathogen human lymphadenitis;
primer probe PCR microarray pathogen human lymphadenitis
IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(B1; multiplex PCR, using ***primers*** specific for IS6110, katG, B1 gene, htrA, ail, inv or fdxA, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; multiplex PCR combined with low-d. microarray technol. for

detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** , gene for; multiplex PCR, using ***primers*** specific for 65-kDa heat shock protein, katG, B1 gene, htrA, ail, inv or fdxA, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT Insertion sequence
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(IS6110; multiplex PCR, using ***primers*** specific for IS6110, katG, B1 gene, htrA, ail, inv or fdxA, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ail; multiplex PCR, using ***primers*** specific for IS6110, katG, B1 gene, htrA, ail, inv or fdxA, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(fdxA; multiplex PCR, using ***primers*** specific for IS6110, katG, B1 gene, htrA, ail, inv or fdxA, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for ***HSP*** ***65*** protein; multiplex PCR, using ***primers*** specific for 65-kDa heat shock protein gene, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(htrA; multiplex PCR, using ***primers*** specific for IS6110, katG, B1 gene, htrA, ail, inv or fdxA, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(inv; multiplex PCR, using ***primers*** specific for IS6110, katG, B1 gene, htrA, ail, inv or fdxA, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(katG; multiplex PCR, using ***primers*** specific for IS6110, katG, B1 gene, htrA, ail, inv or fdxA, combined with low-d. microarray technol. for detecting pathogens in tissues from patients with

granulomatous lymphadenitis)

IT B19 virus
Bartonella henselae
Chlamydia trachomatis
Cytomegalovirus
DNA microarray technology
Human
Human herpesvirus 4
JC virus
Mycobacterium
Toxoplasma gondii
Yersinia
Yersinia enterocolitica
(multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT DNA
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT 937776-05-1D, labeled with Cy3 937776-06-2
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(A. felis fdxA gene-specific ***primer*** ; multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT 937775-97-8D, labeled with Cy5 937775-98-9
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(B. henselae htrA gene-specific ***primer*** ; multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT 937775-93-4 937775-94-5D, labeled with Cy5
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(M. avium katG gene-specific ***primer*** ; multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT 937775-91-2 937775-92-3D, labeled with Cy5
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(M. tuberculosis IS6110-specific ***primer*** ; multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT 937775-99-0D, labeled with Cy5 937776-00-6
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Mycobacterium*** 65-kDa heat shock protein gene-specific ***primer*** ; multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT 937775-95-6D, labeled with Cy3 937775-96-7 937776-07-3 937776-08-4D,
labeled with Cy5
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(T. gondii B1 gene-specific ***primer*** ; multiplex PCR combined

with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT 937776-01-7D, labeled with Cy5 937776-02-8
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Y. enterocolitica ail gene-specific ***primer*** ; multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

IT 937776-03-9D, labeled with Cy5 937776-04-0
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Y. pseudotuberculosis inv gene-specific ***primer*** ; multiplex PCR combined with low-d. microarray technol. for detecting pathogens in tissues from patients with granulomatous lymphadenitis)

L8 ANSWER 12 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2006:1013535 CAPLUS <<LOGINID::20090924>>

DN 146:39451

TI Genetic analysis of ***Mycobacterium*** avium complex strains used for producing purified protein derivatives

AU Semret, Makeda; Bakker, Douwe; Smart, Nonie; Olsen, Ingrid; Haslov, Kaare; Behr, Marcel A.

CS McGill University Health Centre, Montreal, QC, Can.

SO Clinical and Vaccine Immunology (2006), 13(9), 991-996

CODEN: CVILA6; ISSN: 1556-6811

PB American Society for Microbiology

DT Journal

LA English

AB For over a century, purified protein derivs. (PPD) have been used to detect ***mycobacterial*** infections in humans and livestock. Among these, reagents to detect infections by ***Mycobacterium*** avium complex organisms have been produced, but the utility of these reagents has not been clearly established due in part to limited biol. and immunol. standardization. Because there is little information about the strains used to produce these reagents (avian PPD, intracellulare PPD, scrofulaceum PPD, and Johnin), we have performed genetic characterizations of strains used to produce these products. Sequence anal. of 16S rRNA and the hsp65 gene provided results concordant with species designations provided for M. avium, ***Mycobacterium*** intracellulare, and ***Mycobacterium*** scrofulaceum organisms. For M. avium strains, comparative genomic hybridization was performed on a whole-genome DNA microarray, revealing one novel 7.9-kilobase genomic deletion in certain Johnin-producing strains, in addn. to genomic variability inherent to the particular M. avium subspecies. Our findings indicate that considerable genomic differences exist between organisms used for reagents and the infecting organism being studied. These results serve as a baseline for potency studies of different preps. and should aid in comparative studies of newly discovered antigens for the diagnosis of infection and disease by M. avium complex organisms.

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Genetic analysis of ***Mycobacterium*** avium complex strains used for producing purified protein derivatives

AB For over a century, purified protein derivs. (PPD) have been used to detect ***mycobacterial*** infections in humans and livestock. Among these, reagents to detect infections by ***Mycobacterium*** avium

complex organisms have been produced, but the utility of these reagents has not been clearly established due in part. . . products. Sequence anal. of 16S rRNA and the hsp65 gene provided results concordant with species designations provided for *M. avium*, ****Mycobacterium*** intracellulare, and ****Mycobacterium*** scrofulaceum organisms. For *M. avium* strains, comparative genomic hybridization was performed on a whole-genome DNA microarray, revealing one novel 7.9-kilobase. . .**

ST multiplex PCR ****Mycobacterium*** genotyping purified protein deriv IT rRNA*

IT RL: ANT (Analyte); ANST (Analytical study)
(16 S; PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

IT Heat-shock proteins

IT RL: ANT (Analyte); ANST (Analytical study)
(***HSP*** ***65*** , gene hsp65; PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

IT Genotyping (method)

IT ****Mycobacterium*** avium
****Mycobacterium*** intracellulare
****Mycobacterium*** scrofulaceum
(PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)****

IT ***Primers*** (nucleic acid)

IT RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

IT Mutation

IT (deletion, LSPin (large sequence polymorphism); PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

IT Gene, microbial

IT RL: ANT (Analyte); ANST (Analytical study)
(hsp65; PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

IT Microsatellite DNA

IT RL: ANT (Analyte); ANST (Analytical study)
(locus 1, locus 2, locus 8, locus 9; PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

IT Polymerase chain reaction

IT (multiplex; PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

IT Tuberculin

IT RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(purified protein deriv.; PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

IT 916531-71-0 916531-72-1 916531-73-2 916531-74-3 916531-75-4
916531-76-5 916531-77-6 916531-78-7 916531-79-8 916531-80-1
916531-81-2 916531-82-3 916531-83-4 916531-84-5 916531-85-6

IT RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(PCR ***primer*** ; PCR anal. of ****Mycobacterium*** avium complex strains used for producing purified protein derivs.)*

L8 ANSWER 13 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:1460923 CAPLUS <<LOGINID::20090924>>
DN 148:554749
TI Expression and purification of the fusion protein comprising
 Mycobacterium tuberculosis heat shock protein 65 and human
 interleukin 2
AU Wang, Limei; Shi, Changhong; Zhang, Hai; Xue, Ying; Bai, Yinlan; Gao, Hui;
 Xu, Zhikai
CS Department of Microbiology, Fourth of Military Medical University, Xian,
 710032, Peop. Rep. China
SO Zhongguo Renshou Gonghuanbing Xuebao (2006), 22(9), 801-804
CODEN: ZRGXAJ
PB Zhongguo Renshou Gonghuanbing Xuebao Bianweihui
DT Journal
LA Chinese
AB A recombinant plasmid carrying genes coding to ***Mycobacterium***
 tuberculosis hsp65 and human interleukin 2 was constructed and then this
 fusion protein was expressed and purified for use in development of
 vaccine for tuberculosis. Hsp65 gene was amplified by PCR with specific
 primers from the genome of ***Mycobacterium*** tuberculosis
 (MTB) H37Rv and IL-2 gene was amplified from plasmid pGEM-Teasy-IL-2. The
 PCR products were further inserted into pMD18-T vector for sequencing
 hsp65 and IL-2 genes, resp. The EcoRI/ClaI restriction fragment of the IL-2 gene were ligated
 into expression vector pPro-EX HTa and transformed into E. coli
 DH5.alpha.. Then the expressed fusion protein of HSP65-IL-2 was purified
 by Ni-NTA system. Sequence of hsp65 and IL-2 by PCR amplified were
 identical with those of the GenBank reported. Result of SDS-PAGE showed
 that a fusion protein with relative mol. mass (Mr) of 78 kD was expressed,
 which was confirmed by Western-blot anal. with specific monoclonal
 antibody against human IL-2. Thus, this purified fusion proteins obtained
 by Ni-NTA purifn. system. The fusion protein of HSP65-IL-2 constructed
 and expressed in E. coli DH5.alpha. successfully. It may be one of the
 useful candidates for the development of tuberculosis vaccine.
TI Expression and purification of the fusion protein comprising
 Mycobacterium tuberculosis heat shock protein 65 and human
 interleukin 2
AB A recombinant plasmid carrying genes coding to ***Mycobacterium***
 tuberculosis hsp65 and human interleukin 2 was constructed and then this
 fusion protein was expressed and purified for use in development of
 vaccine for tuberculosis. Hsp65 gene was amplified by PCR with specific
 primers from the genome of ***Mycobacterium*** tuberculosis
 (MTB) H37Rv and IL-2 gene was amplified from plasmid pGEM-Teasy-IL-2. The
 PCR products were further inserted into pMD18-T vector. . .
ST ***Mycobacterium*** heat shock protein HSK65 IL2 interleukin
 expression human
IT Heat-shock proteins
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
 (Preparation)
 (***HSP*** ***65*** ; expression and purifn. of fusion protein
 comprising ***Mycobacterium*** tuberculosis heat shock protein 65
 and human interleukin 2)
IT Fusion proteins (chimeric proteins)
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
 (Preparation)
 (HSP65/IL2; expression and purifn. of fusion protein comprising

Mycobacterium tuberculosis heat shock protein 65 and human interleukin 2)

IT Human

Molecular cloning

Mycobacterium tuberculosis (expression and purifn. of fusion protein comprising ***Mycobacterium*** tuberculosis heat shock protein 65 and human interleukin 2)

IT Interleukin 2

RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation) (expression and purifn. of fusion protein comprising ***Mycobacterium*** tuberculosis heat shock protein 65 and human interleukin 2)

IT Plasmid vectors (pMD-hsp65-IL-2; expression and purifn. of fusion protein comprising ***Mycobacterium*** tuberculosis heat shock protein 65 and human interleukin 2)

L8 ANSWER 14 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2006:210283 CAPLUS <>LOGINID::20090924>>

DN 145:434558

TI Sequencing of hsp65 distinguishes among subsets of the ***Mycobacterium*** avium complex

AU Turenne, Christine Y.; Semret, Makeda; Cousins, Debby V.; Collins, Desmond M.; Behr, Marcel A.

CS McGill University Health Centre, Montreal, QC, H3G 1A4, Can.

SO Journal of Clinical Microbiology (2006), 44(2), 433-440

CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB The ***Mycobacterium*** avium complex consists of epidemiol. distinct subsets. The classification of these subsets is complicated by a no. of factors, including the ambiguous results obtained with phenotypic and genetic assays and the recent appreciation that human and avian strains appear to be distinct. In previous work, sequencing based on a 441-bp portion of the hsp65 gene has proven to efficiently classify isolates within the ***Mycobacterium*** genus but provides low resoln. for distinguishing among members of the *M. avium* complex. Therefore, in this study, we have targeted the more variable 3' region of the hsp65 gene to det. whether it can effectively discriminate *M. avium* complex isolates at the levels of species and subspecies. ***Primers*** designed for this target consistently generated amplicons for all organisms classified as *M. avium* complex. Sequences obtained indicate that *M. intracellulare* is genetically divergent from *M. avium* organisms, and distinct sequevars were obtained for *M. avium* subsets, including *M. avium* subsp. *avium* (bird type), *M. avium* subsp. *hominissuis*, and *M. avium* subsp. *paratuberculosis*. In addn., sequence differences served to distinguish bovine from ovine strains of *M. avium* subsp. *paratuberculosis*. A unique profile for *M. avium* subsp. *silvaticum* was not obtained. These results indicate that sequencing the 3' region of the hsp65 gene can simply and unambiguously distinguish species and subspecies of the *M. avium* complex.

OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)

RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Sequencing of hsp65 distinguishes among subsets of the

Mycobacterium avium complex
 AB The ***Mycobacterium*** avium complex consists of epidemiol. distinct subsets. The classification of these subsets is complicated by a no. of factors, including. . . previous work, sequencing based on a 441-bp portion of the hsp65 gene has proven to efficiently classify isolates within the ***Mycobacterium*** genus but provides low resoln. for distinguishing among members of the M. avium complex. Therefore, in this study, we have. . . hsp65 gene to det. whether it can effectively discriminate M. avium complex isolates at the levels of species and subspecies. ***Primers*** designed for this target consistently generated amplicons for all organisms classified as M. avium complex. Sequences obtained indicate that M.. . .

ST ***Mycobacterium*** hsp65 gene sequence phylogeny
 IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (***HSP*** ***65*** ; sequencing of hsp65 distinguishes among subsets of ***Mycobacterium*** avium complex)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (hsp65; sequencing of hsp65 distinguishes among subsets of ***Mycobacterium*** avium complex)

IT Epidemiology
 (mol.; sequencing of hsp65 distinguishes among subsets of ***Mycobacterium*** avium complex)

IT DNA sequences
 Evolution
 Mycobacterium avium
 Mycobacterium avium avium
 Mycobacterium avium hominissuis
 Mycobacterium avium paratuberculosis
 Mycobacterium avium silvaticum
 Mycobacterium chimerae
 Mycobacterium intracellulare

Protein sequences
 (sequencing of hsp65 distinguishes among subsets of ***Mycobacterium*** avium complex)

IT 912708-62-4 912708-64-6 912708-66-8 912708-68-0 912708-70-4
 912708-72-6 912708-74-8 912708-76-0 912708-78-2 912708-80-6
 912708-82-8 912708-84-0 912708-86-2 912708-88-4
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; sequencing of hsp65 distinguishes among subsets of ***Mycobacterium*** avium complex)

IT 912708-61-3 912708-63-5 912708-65-7 912708-67-9 912708-69-1
 912708-71-5 912708-73-7 912708-75-9 912708-77-1 912708-79-3
 912708-81-7 912708-83-9 912708-85-1 912708-87-3
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (nucleotide sequence; sequencing of hsp65 distinguishes among subsets of ***Mycobacterium*** avium complex)

L8 ANSWER 15 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2006:371257 CAPLUS <>LOGINID::20090924>>
 DN 145:432699
 TI Detection of ***mycobacteria*** in Crohn's disease by a broad spectrum

AU polymerase chain reaction
AU Tzen, Chi-Yuan; Wu, Tsu-Yen; Tzen, Chin-Yuan
CS Departments of Pathology, Mackay Memorial Hospital, Taipei, Taiwan
SO Journal of the Formosan Medical Association (2006), 105(4), 290-298
CODEN: JFASEO; ISSN: 0929-6646
PB Elsevier (Singapore) Pte Ltd.
DT Journal
LA English
AB The role of ***mycobacterial*** infection, particularly related to ***Mycobacterium*** avium subsp paratuberculosis (Map), in Crohn's disease has long been debated. We developed ***primer*** pairs capable of detecting a broad spectrum of ***mycobacterium*** and employed them to investigate surgical specimens from patients with Crohn's disease. Pan ***mycobacterium*** ***primers*** specific for the 65-kDa heat shock protein gene (Hsp65) were used in a polymerase chain reaction (PCR) to examine 12 surgically-resected, formalin-fixed, paraffin-embedded specimens from 11 patients with Crohn's disease. The DNA sequences of amplicons were aligned with those in GenBank.
Mycobacterial DNA was found in specimens from three of 11 patients. M. mucogenicum was identified in a specimen from one patient and M. tuberculosis in two, but Map was not identified in any. Hsp65-based PCR can be employed to search for occult ***mycobacterial*** infection of the gastrointestinal tract in patients with a diagnosis or suspicion of Crohn's disease. This approach may have a therapeutic implication.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
TI ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Detection of ***mycobacteria*** in Crohn's disease by a broad spectrum polymerase chain reaction
AB The role of ***mycobacterial*** infection, particularly related to ***Mycobacterium*** avium subsp paratuberculosis (Map), in Crohn's disease has long been debated. We developed ***primer*** pairs capable of detecting a broad spectrum of ***mycobacterium*** and employed them to investigate surgical specimens from patients with Crohn's disease. Pan ***mycobacterium*** ***primers*** specific for the 65-kDa heat shock protein gene (Hsp65) were used in a polymerase chain reaction (PCR) to examine 12. . . formalin-fixed, paraffin-embedded specimens from 11 patients with Crohn's disease. The DNA sequences of amplicons were aligned with those in GenBank. ***Mycobacterial*** DNA was found in specimens from three of 11 patients. M. mucogenicum was identified in a specimen from one patient. . . M. tuberculosis in two, but Map was not identified in any. Hsp65-based PCR can be employed to search for occult ***mycobacterial*** infection of the gastrointestinal tract in patients with a diagnosis or suspicion of Crohn's disease. This approach may have a. . .
ST hsp65 gene specific PCR ***Mycobacterium*** detection Crohn disease;
recA rpoB gene specific PCR ***Mycobacterium*** detection Crohn disease; ***Mycobacterium*** detection Crohn disease hsp65 gene sequence analysis
IT Inflammation
(Crohn's disease; detection of ***Mycobacterium*** mucogenicum and M. tuberculosis in gastrointestinal tract of three Crohn's disease patients using PCR and sequence anal.)
IT Intestine, disease
(Crohn's; detection of ***Mycobacterium*** mucogenicum and M. tuberculosis in gastrointestinal tract of three Crohn's disease

IT patients using PCR and sequence anal.)
Primers (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; detection of ***Mycobacterium*** mucogenicum and M. tuberculosis in gastrointestinal tract of three Crohn's disease patients using hsp65-specific PCR and sequence anal.)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** , gene for; detection of ***Mycobacterium*** mucogenicum in gastrointestinal tract of three Crohn's disease patients using hsp65, recA and rpoB-specific PCRs followed by sequence anal.)

IT Digestive tract
Human
Mycobacterium tuberculosis
PCR (polymerase chain reaction)
(detection of ***Mycobacterium*** mucogenicum and M. tuberculosis in gastrointestinal tract of three Crohn's disease patients using hsp65-specific PCR and sequence anal.)

IT DNA sequences
Mycobacterium mucogenicum
(detection of ***Mycobacterium*** mucogenicum in gastrointestinal tract of three Crohn's disease patients using hsp65, recA and rpoB-specific PCRs followed by sequence anal.)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hsp65; detection of ***Mycobacterium*** mucogenicum and M. tuberculosis in gastrointestinal tract of three Crohn's disease patients using hsp65-specific PCR and sequence anal.)

IT Diagnosis
(mol.; hsp65 gene-specific PCR for detecting occult ***mycobacterial*** infection of gastrointestinal tract in patients with diagnosis or suspicion of Crohn's disease)

IT DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; detection of ***Mycobacterium*** mucogenicum and M. tuberculosis in gastrointestinal tract of three Crohn's disease patients using hsp65-specific PCR and sequence anal.)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(recA; detection of ***Mycobacterium*** mucogenicum in gastrointestinal tract of three Crohn's disease patients using hsp65, recA and rpoB-specific PCRs followed by sequence anal.)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rpoB; detection of ***Mycobacterium*** mucogenicum in gastrointestinal tract of three Crohn's disease patients using hsp65,

recA and rpoB-specific PCRs followed by sequence anal.)

IT 912984-86-2 912984-87-3
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hsp65 gene-specific ***primer*** ; detection of
Mycobacterium mucogenicum in gastrointestinal tract of three Crohn's disease patients using hsp65, recA and rpoB-specific PCRs followed by sequence anal.)

IT 912984-88-4 912984-89-5
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(recA gene-specific ***primer*** ; detection of
Mycobacterium mucogenicum in gastrointestinal tract of three Crohn's disease patients using hsp65, recA and rpoB-specific PCRs followed by sequence anal.)

IT 912984-90-8 912984-91-9
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rpoB gene-specific ***primer*** ; detection of
Mycobacterium mucogenicum in gastrointestinal tract of three Crohn's disease patients using hsp65, recA and rpoB-specific PCRs followed by sequence anal.)

L8 ANSWER 16 OF 42 MEDLINE on STN
AN 2007174630 MEDLINE <>LOGINID::20090924>>
DN PubMed ID: 17373358
TI Characterization of ***mycobacteria*** isolated from bovines by PRA-targetting ***hsp*** ***65*** gene region.
AU Parashar Deepti; Srivastava R K; Chauhan D S; Sharma V D; Singh Mradula; Lavania Mallika; Chauhan Aradhana; Bhatia A K; Katoch V M
CS Deptt of Microbiology and Molecular Biology, National JALMA Institute for Leprosy and Other Mycobacterial Diseases (ICMR), Tajganj, Agra 282001.
SO The Journal of communicable diseases, (2006 Mar) Vol. 38, No. 3, pp. 263-8.
Journal code: 0261652. ISSN: 0019-5138.
CY India
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200704
ED Entered STN: 24 Mar 2007
Last Updated on STN: 27 Apr 2007
Entered Medline: 26 Apr 2007
AB Bovine tuberculosis caused by the bacterium ***Mycobacterium*** bovis is a major infectious disease of animals and has zoonotic importance for humans. Even though the incidence is believed to be very low in India, human tuberculosis caused by M. bovis has been increasingly recognized in many other countries of the world. As differentiation of ***mycobacterial*** species take long time, a method for the rapid identification of ***mycobacteria*** isolated from bovine samples to the species level was used, which is based on polymerase chain reaction (PCR) of the gene encoding for the 65-kD protein followed by restriction analysis. The method involves restriction enzyme analysis of PCR products

obtained with ***primers*** common to all ***mycobacteria*** and generate M. tuberculosis complex specific pattern. PRA was performed on 33 bovine isolates of which 90.9% (30/33) isolates were identified clearly as M. tuberculosis complex, M. fortuitum, M. phlei and M. smegmatis using restriction enzyme Hae III.

TI Characterization of ***mycobacteria*** isolated from bovines by PRA-targetting ***hsp*** ***65*** gene region.

AB Bovine tuberculosis caused by the bacterium ***Mycobacterium*** bovis is a major infectious disease of animals and has zoonotic importance for humans. Even though the incidence is believed. . . human tuberculosis caused by M. bovis has been increasingly recognized in many other countries of the world. As differentiation of ***mycobacterial*** species take long time, a method for the rapid identification of ***mycobacteria*** isolated from bovine samples to the species level was used, which is based on polymerase chain reaction (PCR) of the. . . encoding for the 65-kD protein followed by restriction analysis. The method involves restriction enzyme analysis of PCR products obtained with ***primers*** common to all ***mycobacteria*** and generate M. tuberculosis complex specific pattern. PRA was performed on 33 bovine isolates of which 90.9% (30/33) isolates were. . .

CT Animals

*Bacterial Proteins: CL, classification

Bacterial Proteins: GE, genetics

Cattle

*Chaperonins: CL, classification

Chaperonins: GE, genetics

DNA, Bacterial: AN, analysis

****Mycobacteria, Atypical: CL, classification***

*** Mycobacteria, Atypical: GE, genetics***

****Mycobacterium phlei: CL, classification***

*** Mycobacterium phlei: GE, genetics***

****Mycobacterium tuberculosis: CL, classification***

*** Mycobacterium tuberculosis: GE, genetics***

Polymerase Chain Reaction: MT, methods

*Polymorphism, Restriction Fragment Length

*Tuberculosis, Bovine: CL, classification

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA, Bacterial); 0 (heat-shock protein 65, ***Mycobacterium***)

L8 ANSWER 17 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2007:43138 CAPLUS <<LOGINID::20090924>>

DN 146:398734

TI Pathological and molecular studies on ***mycobacteriosis*** of milkfish Chanos chanos in Taiwan

AU Chang, Tsung-Chou; Hsieh, Chia-Yu; Chang, Ching-Dong; Shen, Ying-Ling; Huang, Kwo-Ching; Tu, Chien; Chen, Li-Chun; Wu, Zong-Bing; Tsai, Shinn-Shyong

CS Department of Veterinary Medicine, National Pingtung University of Science and Technology, Pingtung, 192, Taiwan

SO Diseases of Aquatic Organisms (2006), 72(2), 147-151

CODEN: DAOREO; ISSN: 0177-5103

PB Inter-Research

DT Journal

LA English

AB An outbreak of ***mycobacteriosis*** was investigated in milkfish Chanos chanos, which had a cumulative mortality of .ltoreq.66.7% over the

course of 1 yr. Gross reddish- or greyish-white nodules appeared on the peritoneal surface, spleen, kidney, liver and gastrointestinal (GI) tract. Epithelioid granulomas with the formation of Langhan's type giant cells were the prominent histopathol. changes. Despite large nos. of acid-fast bacilli in the granulomas, neither caseous necrosis nor dystrophic calcification were obsd. Using degenerate ***primers*** that targeted the heat shock protein 65 kDa gene of ***Mycobacterium*** spp., a 441 bp product was amplified. When compared with published sequences, our products were identical to those of ***Mycobacterium*** abscessus Type II. This is the 1st report of *M. abscessus* infection in milkfish.

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

- TI Pathological and molecular studies on ***mycobacteriosis*** of milkfish *Chanos chanos* in Taiwan
- AB An outbreak of ***mycobacteriosis*** was investigated in milkfish *Chanos chanos*, which had a cumulative mortality of .ltoreq.66.7% over the course of 1 yr. Gross. . . changes. Despite large nos. of acid-fast bacilli in the granulomas, neither caseous necrosis nor dystrophic calcification were obsd. Using degenerate ***primers*** that targeted the heat shock protein 65 kDa gene of ***Mycobacterium*** spp., a 441 bp product was amplified. When compared with published sequences, our products were identical to those of ***Mycobacterium*** abscessus Type II. This is the 1st report of *M. abscessus* infection in milkfish.
- ST milkfish ***Mycobacterium*** infection
- IT Air bladder
Aquaculture
Bacterial infection
Chanos chanos
DNA sequences
Digestive tract
Granuloma
Kidney
Liver
Mycobacterium abscessus
Peritoneum
Protein sequences
Spleen
(DNA sequence indicates ***Mycobacterium*** abscessus infection of milkfish in Taiwan)
- IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** ***65*** ; DNA sequence indicates ***Mycobacterium*** abscessus infection of milkfish in Taiwan)
- IT 933811-51-9, GenBank AAY79349
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; DNA sequence indicates ***Mycobacterium*** abscessus infection of milkfish in Taiwan)
- IT 933811-50-8, GenBank DQ067577
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; DNA sequence indicates ***Mycobacterium*** abscessus infection of milkfish in Taiwan)

DN 146:177739
TI Rapid detection and species identification of ***Mycobacterium*** spp.
using real-time PCR and DNA-Microarray
AU Tobler, Nadia E.; Pfunder, Monika; Herzog, Katrin; Frey, Juerg E.;
Altwegg, Martin
CS Institute of Medical Microbiology, University of Zurich, Zurich, CH-8028,
Switz.
SO Journal of Microbiological Methods (2006), 66(1), 116-124
CODEN: JMIMDQ; ISSN: 0167-7012
PB Elsevier B.V.
DT Journal
LA English
AB Infections with ***mycobacteria*** are an important issue in public health care. Here we present a proof-of-principle' concept for the identification of 37 different ***Mycobacterium*** species using 5' exonuclease real-time PCR and DNA microarray based on the region upstream of the 65 kDa heat shock protein. With our two PCR probes, one complementary to all ***mycobacteria*** species, the other specific for the M. tbc-complex, 34 species were properly classified by real-time PCR. After reamplification and hybridization to a DNA microarray, all species showed a specific pattern. All 10 blindly tested pos. cultures revealed a pos. real-time PCR signal with the genus probe. After reamplification and hybridization, six samples could unambiguously be identified. One sample showed a mixt. of presumably three species-specific patterns and sequencing the 16S rRNA confirmed the presence of a mixt. The hybridization results of three specimens could not be interpreted because the signal to background ratio was not sufficient. Two samples considered as neg. controls (LAL Reagent Water (Cambrex) and DNA of Candida albicans) gave neither a genus nor a M. tbc-complex pos. PCR signal. Based on these results we consider our method to be a promising tool for the rapid identification of different ***mycobacteria*** species, with the advantage of possible identification of mixed infections or contaminations.

OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Rapid detection and species identification of ***Mycobacterium*** spp.
using real-time PCR and DNA-Microarray
AB Infections with ***mycobacteria*** are an important issue in public health care. Here we present a proof-of-principle' concept for the identification of 37 different ***Mycobacterium*** species using 5' exonuclease real-time PCR and DNA microarray based on the region upstream of the 65 kDa heat shock protein. With our two PCR probes, one complementary to all ***mycobacteria*** species, the other specific for the M. tbc-complex, 34 species were properly classified by real-time PCR. After reamplification and hybridization. . . signal. Based on these results we consider our method to be a promising tool for the rapid identification of different ***mycobacteria*** species, with the advantage of possible identification of mixed infections or contaminations.

ST real time PCR DNA microarray HSP65 ***Mycobacterium*** species
identification; ***Mycobacterium*** species identification detection
primer probe HSP65
IT ***Primers*** (nucleic acid)

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(DNA, 65kDaf2, 65KDar3 and 65kDar4; description of a two-step procedure (real-time PCR and DNA microarray) for identification of 37 different ***Mycobacterium*** species based on upstream HSP65 gene sequence)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** , gene for; rapid detection and species identification of ***Mycobacterium*** spp. using HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT ***Mycobacterium***
(description of a two-step procedure (real-time PCR and DNA microarray) for identification of 37 different ***Mycobacterium*** species based on upstream HSP65 gene sequence)

IT DNA microarray technology
Mycobacterium tuberculosis
(description of a two-step procedure (real-time PCR and DNA microarray) for identification of 37 different ***Mycobacterium*** species based on upstream HSP65 gene sequence, including ***Mycobacterium*** tuberculosis)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for HSP65, upstream region; description of a two-step procedure (real-time PCR and DNA microarray) for identification of 37 different ***Mycobacterium*** species based on upstream HSP65 gene sequence)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(labeled with FAM, Cy3, Dabcyl or BHQ2; description of a two-step procedure (real-time PCR and DNA microarray) for identification of 37 different ***Mycobacterium*** species based on upstream HSP65 gene sequence)

IT Diagnosis
(mol.; description of a two-step procedure (real-time PCR and DNA microarray) for identification of 37 different ***Mycobacterium*** species based on upstream HSP65 gene sequence, including ***Mycobacterium*** tuberculosis)

IT DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** , 65kDaf2, 65KDar3 and 65kDar4; description of a two-step procedure (real-time PCR and DNA microarray) for identification of 37 different ***Mycobacterium*** species based on upstream HSP65 gene sequence)

IT Polymerase chain reaction
(real-time; rapid detection and species identification of ***Mycobacterium*** spp. using HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT 919130-80-6
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** 65KDar3; rapid detection and species identification of ***Mycobacterium*** spp. using HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT 919130-79-3

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** 65kDaf2; rapid detection and species identification of ***Mycobacterium*** spp. using HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT 919130-81-7
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** 65kDar4; rapid detection and species identification of ***Mycobacterium*** spp. using HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT 919130-82-8D, 5'-labeled with FAM and 3'-labeled with Dabcyl
919130-83-9D, 5'-labeled with Cy3 and 3'-labeled with BHQ-2
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe; rapid detection and species identification of ***Mycobacterium*** spp. using HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT 6268-49-1D, Dabcyl, oligonucleotide conjugate 76823-03-5D, FAM, oligonucleotide conjugate 146368-16-3D, Cy3, oligonucleotide conjugate 374591-96-5D, BHQ-2, oligonucleotide conjugate
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rapid detection and species identification of ***Mycobacterium*** spp. using HSP65 gene-specific real-time PCR and DNA microarray technol.)

L8 ANSWER 19 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:158391 CAPLUS <>LOGINID::20090924>>
DN 145:263808
TI Identification of ***Mycobacterium*** marinum 65 kD heat shock protein gene by polymerase chain reaction restriction analysis from lesions of swimming pool granuloma
AU Cai, Lin; Xue, Chen; Zhao, Ting; Ding, Bei-chuan; Zhang, Jian-zhong
CS Department of Dermatology, Peking University People's Hospital, Beijing, 100044, Peop. Rep. China
SO Chinese Medical Journal (Beijing, China, English Edition) (2006), 119(1), 43-48
CODEN: CMJODS; ISSN: 0366-6999
PB Chinese Medical Association
DT Journal
LA English
AB Nontuberculous ***mycobacterium*** (NTM) had been reported to cause cutaneous infections which are difficult to interpret due to the variability of the clin. manifestations. Among NTM infections, ***Mycobacterium*** marinum (M. marinum) are mostly seen to cause skin infection. It is therefore important to establish a rapid approach for detection and identification of M. marinum from lesions of patients with suspected M. marinum infections. Specimens were obtained from 5 patients with swimming pool granuloma. DNA was extd. and polymerase chain reaction (PCR) was performed. PCR products were digested with Hae III and BstE II, then analyzed by pattern restriction anal. to detect heat shock protein (***hsp***) ***65*** kD gene. The 65 kD hsp gene was found in all

specimens from patients with swimming pool granuloma. PCR restriction anal. (PRA) identified all 5 samples to be *M. marinum* infections, and the result was consistent with that of routine bacteriol. identification. The lesions subsided or markedly improved upon treatment. The authors conclude that PRA is a sensitive, specific and rapid method in identification of ***mycobacteria*** . Application of this method will be helpful for early diagnosis of ***mycobacterial*** skin infections.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

- TI Identification of ****Mycobacterium**** *marinum* 65 kD heat shock protein gene by polymerase chain reaction restriction analysis from lesions of swimming pool granuloma
- AB Nontuberculous ****Mycobacterium**** (NTM) had been reported to cause cutaneous infections which are difficult to interpret due to the variability of the clin. manifestations. Among NTM infections, ****Mycobacterium**** *marinum* (*M. marinum*) are mostly seen to cause skin infection. It is therefore important to establish a rapid approach for. . . products were digested with Hae III and BstE II, then analyzed by pattern restriction anal. to detect heat shock protein (***hsp***) ***65*** kD gene. The 65 kD hsp gene was found in all specimens from patients with swimming pool granuloma. PCR restriction. . . or markedly improved upon treatment. The authors conclude that PRA is a sensitive, specific and rapid method in identification of ***mycobacteria*** . Application of this method will be helpful for early diagnosis of ***mycobacterial*** skin infections.
- ST gene hsp65 specific PCR ****Mycobacterium**** detection human granuloma; PCR restriction enzyme analysis hsp65 specific ****Mycobacterium**** detection
- IT PCR (polymerase chain reaction)
(-restriction enzyme anal.; gene hsp65-specific PCR followed by restriction enzyme anal. (PRA) used to identify ****Mycobacterium**** *marinum* in lesions from patients with swimming pool granuloma)
- IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA, Tb11 and Tb12; gene hsp65-specific PCR followed by restriction enzyme anal. (PRA) used to identify ****Mycobacterium**** *marinum* in lesions from patients with swimming pool granuloma)
- IT Human
****Mycobacterium**** *marinum*
(gene hsp65-specific PCR followed by restriction enzyme anal. (PRA) used to identify ****Mycobacterium**** *marinum* in lesions from patients with swimming pool granuloma)
- IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hsp65; gene hsp65-specific PCR followed by restriction enzyme anal. (PRA) used to identify ****Mycobacterium**** *marinum* in lesions from patients with swimming pool granuloma)
- IT Skin, disease
(lesion; gene hsp65-specific PCR followed by restriction enzyme anal. (PRA) used to identify ****Mycobacterium**** *marinum* in lesions from patients with swimming pool granuloma)
- IT Diagnosis
(mol.; gene hsp65-specific PCR followed by restriction enzyme anal. (PRA) used to identify ****Mycobacterium**** *marinum* in lesions from patients with swimming pool granuloma)

IT DNA
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** , Tb11 and Tb12; gene hsp65-specific PCR followed by
restriction enzyme anal. (PRA) used to identify ***Mycobacterium***
marinum in lesions from patients with swimming pool granuloma)

IT Granuloma
(swimming pool; gene hsp65-specific PCR followed by restriction enzyme
anal. (PRA) used to identify ***Mycobacterium*** marinum in lesions
from patients with swimming pool granuloma)

L8 ANSWER 20 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:986878 CAPLUS <>LOGINID::20090924>>
DN 146:352092
TI Development of PCR-RFLP for identification of eight ***mycobacterial***
species
AU Li, Xiaojie; Wang, Hongsheng; Wu, Qinxue; Cui, Pangen; Liu, Xunquan
CS Institute of Dermatology, Chinese Academy of Medical Sciences and Peking
Union Medical College, Nanjing, 210042, Peop. Rep. China
SO Zhonghua Pifuke Zazhi (2005), 38(9), 533-535
CODEN: CHFTAJ; ISSN: 0412-4030
PB Zhongguo Yixue Kexueyuan Pifubing Yanjiuso
DT Journal
LA Chinese
AB A PCR-RFLP method for the identification of eight ***mycobacterial***
species was developed. PCR was performed targeting the gene encoding
65-kDa heat shock protein which was common to all ***mycobacteria*** .
Two restriction enzymes, BstE II and Hae III, were used to digest the PCR
products, and specific restriction patterns of different
mycobacteria were obtained. The specific restriction patterns of
different ***mycobacteria*** were identical to the data previously
reported. M. avium, M. intracellulare, M. kansasii, M. tuberculosis, M.
scrofulaceum, M. marinum, M. fortuitum and M. chelonae could be
differentiated in one expt. by PCR-RFLP.
TI Development of PCR-RFLP for identification of eight ***mycobacterial***
species
AB A PCR-RFLP method for the identification of eight ***mycobacterial***
species was developed. PCR was performed targeting the gene encoding
65-kDa heat shock protein which was common to all ***mycobacteria*** .
Two restriction enzymes, BstE II and Hae III, were used to digest the PCR
products, and specific restriction patterns of different
mycobacteria were obtained. The specific restriction patterns of
different ***mycobacteria*** were identical to the data previously
reported. M. avium, M. intracellulare, M. kansasii, M. tuberculosis, M.
scrofulaceum, M. marinum, M.. . .
ST ***Mycobacterium*** heat shock protein 65 PCR RFLP; PCR RFLP detection
Mycobacterium heat shock protein hsp65 gene
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** ; PCR-RFLP for identification of
Mycobacterial species)
IT ***Mycobacterium*** avium
Mycobacterium chelonae
Mycobacterium fortuitum
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium marinum

Mycobacterium scrofulaceum
Mycobacterium tuberculosis

Polymerase chain reaction
Restriction fragment length polymorphism
(PCR-RFLP for identification of ***Mycobacterial*** species)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(hsp65; PCR-RFLP for identification of ***Mycobacterial*** species)

IT Diagnosis
(mol.; PCR-RFLP for identification of ***Mycobacterial*** species)

IT 930134-85-3 930134-86-4
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; PCR-RFLP for identification of ***Mycobacterial*** species)

IT 81295-18-3 93229-61-9, Restriction endonuclease, BstE II
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR-RFLP for identification of ***Mycobacterial*** species)

L8 ANSWER 21 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:620828 CAPLUS <>LOGINID:>:20090924>>
DN 144:206426

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (hsp65) gene for differentiation of ***Mycobacterium*** spp.

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Bum-Joon

CS Department of Microbiology and Liver Research Institute, College of Medicine, Seoul National University Chongno-gu, 28 Yongon-dong, Chongno-gu, Seoul, 110-799, S. Korea

SO Journal of Microbiological Methods (2005), 62(2), 199-209
CODEN: JMIMDQ; ISSN: 0167-7012

PB Elsevier B.V.

DT Journal

LA English

AB A method based on PCR-restriction fragment length polymorphism anal. (PRA) using a novel region of the hsp65 gene was developed for the rapid and exact identification of ***mycobacteria*** to the species level. A 644 bp region of hsp65 in 62 ***mycobacteria*** ref. strains, and 4 related bacterial strains was amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, AvaII, HphI, and HpaII. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the sepn. of *M. avium*, *M. intracellulare* and *M. tuberculosis* to the species level by AvaII digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clin. isolates, which had been characterized by conventional biochem. testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of ***mycobacteria*** culture isolates at the species level.

OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm

targeting 644 bp Heat Shock Protein 65 (hsp65) gene for differentiation of ***Mycobacterium*** spp.

AB . . . polymorphism anal. (PRA) using a novel region of the hsp65 gene was developed for the rapid and exact identification of ***mycobacteria*** to the species level. A 644 bp region of hsp65 in 62 ***mycobacteria*** ref. strains, and 4 related bacterial strains was amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, AvaiII, HphI, and HpaII. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the sepn. of . . . biochem. testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of ***mycobacteria*** culture isolates at the species level.

ST PCR RFLP algorithm hsp65 gene restriction endonuclease ***Mycobacterium***

IT Heat-shock proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(***HSP*** ***65*** ; PCR RFLP algorithm, targeting hsp65 gene, for identification of ***Mycobacterium*** in clin. isolates)

IT Algorithm
Human
Mycobacterium
Mycobacterium avium
Mycobacterium intracellulare
Mycobacterium tuberculosis
PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(PCR RFLP algorithm, targeting hsp65 gene, for identification of ***Mycobacterium*** in clin. isolates)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR; PCR RFLP algorithm, targeting hsp65 gene, for identification of ***Mycobacterium*** in clin. isolates)

IT 81295-07-0, Restriction endonuclease AvaiII 81295-25-2, Restriction endonuclease HpaII 81295-26-3, Restriction endonuclease HphI
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(PCR RFLP algorithm, targeting hsp65 gene, for identification of ***Mycobacterium*** in clin. isolates)

IT 875804-98-1
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** HSPF3; PCR RFLP algorithm, targeting hsp65 gene, for identification of ***Mycobacterium*** in clin. isolates)

IT 875804-99-2
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** HSPR4; PCR RFLP algorithm, targeting hsp65 gene, for identification of ***Mycobacterium*** in clin. isolates)

L8 ANSWER 22 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:810645 CAPLUS <<LOGINID::20090924>>
DN 144:49294
TI ***Mycobacterium*** tuberculosis complex DNA does not exist in

AU atheromatous plaques
AU Rota, Simin; Tuncer, S.; Rota, S.; Kanat, O.
CS Pamukkale University Medical School Department of Biochemistry, Denizli,
Turk.
SO New Microbiologica (2005), 28(2), 165-169
CODEN: NMEIB2; ISSN: 1121-7138
PB Edizioni Internazionali srl, Div. EDIMES
DT Journal
LA English
AB The possible potential role of several infectious agents in
atherosclerosis has been shown. Several infectious agents DNA in
atheromatous plaques have been displayed by PCR. In patients with
atheromas antibody levels against Hsp65 were higher. Vaccination of mice
with recombinant Hsp65 and Hsp65-rich M. tuberculosis resulted in
formation of atheromatous plaques. We attempted to detect M. tuberculosis
DNA in atherosclerotic plaque samples by PCR. In endarterectomy tissue
samples obtained from patients during coronary artery bypass graft surgery
DNA was prep'd. by proteinase-K digestion, phenol/chloroform extn. and
ethanol pptn. After amplification with M.tuberculosis complex IS6110
region specific ***primers***, the products were analyzed on
electrophoresis. M. tuberculosis DNA was neg. in all tissue samples.
More data on etiol. studies with ***mycobacteriaceae*** will be yield
information on atherosclerosis pathogenesis.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI ***Mycobacterium*** tuberculosis complex DNA does not exist in
atheromatous plaques
AB . . . surgery DNA was prep'd. by proteinase-K digestion,
phenol/chloroform extn. and ethanol pptn. After amplification with
M.tuberculosis complex IS6110 region specific ***primers***, the
products were analyzed on electrophoresis. M. tuberculosis DNA was neg.
in all tissue samples. More data on etiol. studies with
mycobacteriaceae will be yield information on atherosclerosis
pathogenesis.
ST ***Mycobacterium*** tuberculosis DNA atherosclerosis
IT Heat-shock proteins
RL: ADV (Adverse effect, including toxicity); BSU (Biological study,
unclassified); BIOL (Biological study)
(***HSP*** ***65*** ; ***Mycobacterium*** tuberculosis
complex DNA does not exist in atheromatous plaques)
IT DNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***Mycobacterium*** tuberculosis complex DNA does not exist in
atheromatous plaques)
IT Atherosclerosis
Coronary bypass surgery
Heart
Human
Mycobacterium tuberculosis
(polymerase chain reaction technique showed ***Mycobacterium***
tuberculosis complex IS6110 region DNA did not exist in atherosclerotic
plaque sample obtained from patient undergoing coronary artery bypass
graft surgery)
L8 ANSWER 23 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:81792 CAPLUS <<LOGINID::20090924>>

DN 143:20521
TI Rapid species identification within the ***Mycobacterium*** chelonae-abscessus group by high-resolution melting analysis of hsp65 PCR products
AU Odell, Ian D.; Cloud, Joann L.; Seipp, Michael; Wittwer, Carl T.
CS Department of Pathology, University of Utah Medical School, Salt Lake City, USA
SO American Journal of Clinical Pathology (2005), 123(1), 96-101
CODEN: AJCPAI; ISSN: 0002-9173
PB American Society of Clinical Pathology
DT Journal
LA English
AB Polymerase chain reaction (PCR) amplification of the heat shock protein 65 (hsp65) gene followed by high-resoln. melting anal. with LCGreen I (Idaho Technol., Salt Lake City, UT) was used to differentiate the ***mycobacteria*** species ***Mycobacterium*** chelonae, ***Mycobacterium*** abscessus, and ***Mycobacterium*** immunogenum in less than 20 min. A 105-base-pair amplicon that clustered the different species by predicted melting temp. was found from available GenBank hsp65 sequences. We identified 24 clin. isolates within the M chelonae-abscessus group by proximal 16S rRNA and hsp65 gene sequencing. Rapid-cycle PCR followed by high-resoln. melting anal. clustered these samples into the following groups: M abscessus, 12; M abscessus sequence variant, 2; M chelonae, 7; unexpected M chelonae sequence variant, 1; and M immunogenum, 2. The M chelonae variant had a single base change not found in reported GenBank sequences. Advantages of the method include speed, low risk of amplicon contamination (closed-tube), and no need for sepn. steps (sequencing, electrophoresis, high-performance liq. chromatog.) or real-time monitoring.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Rapid species identification within the ***Mycobacterium*** chelonae-abscessus group by high-resolution melting analysis of hsp65 PCR products
AB . . . gene followed by high-resoln. melting anal. with LCGreen I (Idaho Technol., Salt Lake City, UT) was used to differentiate the ***mycobacteria*** species ***Mycobacterium*** chelonae, ***Mycobacterium*** abscessus, and ***Mycobacterium*** immunogenum in less than 20 min. A 105-base-pair amplicon that clustered the different species by predicted melting temp. was found. . .
ST PCR melting analysis ***Mycobacterium*** gene hsp65
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** ; species identification within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of hsp65 PCR products)
IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hsp65; species identification within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of hsp65 PCR products)
IT Nucleic acid hybridization
(melting anal.; species identification within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of hsp65 PCR products)

IT Diagnosis
(mol.; species identification within ***Mycobacterium***
chelonae-abscessus group by high-resoln. melting anal. of hsp65 PCR
products)

IT Human
Mycobacterium abscessus
Mycobacterium chelonae
Mycobacterium immunogenum

PCR (polymerase chain reaction)
(species identification within ***Mycobacterium***
chelonae-abscessus group by high-resoln. melting anal. of hsp65 PCR
products)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(species identification within ***Mycobacterium***
chelonae-abscessus group by high-resoln. melting anal. of hsp65 PCR
products)

IT Genotyping (method)
(species identification; species identification within
Mycobacterium chelonae-abscessus group by high-resoln. melting
anal. of hsp65 PCR products)

IT 853031-88-6 853031-89-7
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; species identification within
Mycobacterium chelonae-abscessus group by high-resoln. melting
anal. of hsp65 PCR products)

L8 ANSWER 24 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:69709 CAPLUS <<LOGINID::20090924>>
DN 143:1806
TI A new method for species identification and differentiation of
Mycobacterium chelonae complex based on amplified hsp65
restriction analysis (AHSPRA)
AU Selvaraju, Suresh B.; Khan, Izhar U. H.; Yadav, Jagjit S.
CS Molecular Toxicology Division, Department of Environmental Health,
University of Cincinnati Medical Center, Cincinnati, OH, 45267-0056, USA
SO Molecular and Cellular Probes (2005), 19(2), 93-99
CODEN: MCPRE6; ISSN: 0890-8508
PB Elsevier B.V.
DT Journal
LA English
AB Members of the ***Mycobacterium*** chelonae complex (MCC), namely M.
chelonae, ***Mycobacterium*** abscessus and ***Mycobacterium***
immunogenum, have been implicated in nosocomial infections and
occupational respiratory illnesses like hypersensitivity pneumonitis (HP)
assocd. with contaminated metalworking fluid (MWF) exposures. Close
relationship among these member species makes their differentiation
cumbersome using the existing methods. Here we report a simple and rapid
method for unambiguous identification and differentiation of the
three-member species of the MCC group with PCR-restriction anal. targeting
a 667-bp segment of a variable region of the 65-kDa-heat shock protein
(hsp65) gene. This assay, described as Amplified hsp65 Restriction Anal.
(AHSPRA), can discriminate all the three individual species using a
one-step restriction digestion using either BbvI or Eco0109I. The enzyme
NarI can differentiate M. immunogenum from the other two MCC species (M.

chelonae and M. abscessus). The developed method was validated using several non-MCC ref. species of other rapidly growing ***mycobacteria*** (RGM) and MCC field isolates from MWF samples. Direct cell-lysis was used instead of the conventional DNA template prepn., which improved the rapidity, simplicity and adaptability of the developed method. The results suggest that the developed method can unambiguously differentiate species of the M. chelonae complex from other RGM species and from one another.

OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI A new method for species identification and differentiation of ***Mycobacterium*** chelonae complex based on amplified hsp65 restriction analysis (AHSPRA)

AB Members of the ***Mycobacterium*** chelonae complex (MCC), namely M. chelonae, ***Mycobacterium*** abscessus and ***Mycobacterium*** immunogenum, have been implicated in nosocomial infections and occupational respiratory illnesses like hypersensitivity pneumonitis (HP) assocd. with contaminated metalworking fluid. . . . species (M. chelonae and M. abscessus). The developed method was validated using several non-MCC ref. species of other rapidly growing ***mycobacteria*** (RGM) and MCC field isolates from MWF samples. Direct cell-lysis was used instead of the conventional DNA template prepn., which. . . .

ST sequence ***Mycobacterium*** gene hsp65 PCR diagnosis

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(***HSP*** ***65*** ; PCR method for species identification and differentiation of ***Mycobacterium*** chelonae complex based on gene hsp65)

IT DNA sequences

Mycobacterium abscessus

Mycobacterium chelonae

Mycobacterium immunogenum

PCR (polymerase chain reaction)

Protein sequences

RFLP (restriction fragment length polymorphism)

Respiratory system, disease

(PCR method for species identification and differentiation of ***Mycobacterium*** chelonae complex based on gene hsp65)

IT ***Primers*** (nucleic acid)

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(PCR method for species identification and differentiation of ***Mycobacterium*** chelonae complex based on gene hsp65)

IT Human

(diagnosis in; PCR method for species identification and differentiation of ***Mycobacterium*** chelonae complex based on gene hsp65)

IT Gene, microbial

RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(hsp65; PCR method for species identification and differentiation of ***Mycobacterium*** chelonae complex based on gene hsp65)

IT Diagnosis

(mol.; PCR method for species identification and differentiation of

Mycobacterium chelonae complex based on gene hsp65)
IT 852345-32-5 852345-33-6
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; PCR method for species identification and
differentiation of ***Mycobacterium*** chelonae complex based on
gene hsp65)
IT 824883-12-7 824883-14-9 824883-16-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; PCR method for species identification and
differentiation of ***Mycobacterium*** chelonae complex based on
gene hsp65)
IT 824883-11-6 824883-13-8 824883-15-0
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic
use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
USES (Uses)
(nucleotide sequence; PCR method for species identification and
differentiation of ***Mycobacterium*** chelonae complex based on
gene hsp65)

L8 ANSWER 25 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:1008663 CAPLUS <>LOGINID::20090924>>
DN 144:348656
TI Construction and sequencing of recombinant T helper multi-epitope gene
plasmid
AU Gao, Wenjun; Wei, Min; Peng, Xiaomou; Gao, Zhiliang
CS Department of Infection, Zhongshan People's Hospital, Zhongshan, Guangdong
Province, 528400, Peop. Rep. China
SO Xinxiang Yixueyuan Xuebao (2005), 22(1), 4-6, 10
CODEN: XYIXEQ; ISSN: 1004-7239
PB Xinxiang Yixueyuan Xuebao Bianji Weiyuanhui
DT Journal
LA Chinese
AB Objective: Th multi-epitope gene was made. Methods: Th multi-epitope
peptide was made up of 5 Th epitopes (heat shock protein 65 of
Mycobacterium tuberculosis pl-20, E2 protein of Rubella virus
p54-65, engineering epitope PADRE, heat shock protein 60 of Chlamydia
trachomatis p35-48, and tetanus toxin p830-843). Four 69 bp
oligonucleotides overlapping by 19 bp and a pair of ***primers*** were
synthesized according to the sequence of the Th multi-epitope. The four
oligonucleotides were spliced together by using splicing by overlap
extension (SOE). The splicing products were cloned into PUC18 and checked
for mutations by sequencing. Results: The Th multi-epitope gene was made
by using SOE. A recombinant plasmid was constructed. Conclusion: The
successful construction of the Th multi-epitope gene lays a foundation for
constructing high effective Th multi-epitope vaccines.
AB . . . multi-epitope gene was made. Methods: Th multi-epitope peptide
was made up of 5 Th epitopes (heat shock protein 65 of
Mycobacterium tuberculosis pl-20, E2 protein of Rubella virus
p54-65, engineering epitope PADRE, heat shock protein 60 of Chlamydia
trachomatis p35-48, and tetanus toxin p830-843). Four 69 bp
oligonucleotides overlapping by 19 bp and a pair of ***primers*** were
synthesized according to the sequence of the Th multi-epitope. The four
oligonucleotides were spliced together by using splicing by . . .
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)

(***HSP*** ***65*** , ***Mycobacterium*** tuberculosis
pl-20, epitope; construction of recombinant T helper chimeric
multi-epitope gene)

L8 ANSWER 26 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:727349 CAPLUS <>LOGINID::20090924>>
DN 142:87110
TI Capillary electrophoretic restriction fragment length polymorphism
patterns for the ***mycobacterial*** hsp65 gene
AU Ho, Hsin-Tsung; Chang, Po-Ling; Hung, Chia-Chien; Chang, Huan-Tsung
CS Department of Laboratory Medicine, Mackay Memorial Hospital, Taipei,
Taiwan
SO Journal of Clinical Microbiology (2004), 42(8), 3525-3531
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB PCR-restriction fragment length polymorphism (RFLP) anal. is a nonprobe
method for the rapid identification of ***Mycobacterium*** species.
We demonstrate the sepn. of DNA or restriction fragments digested from the
mycobacterial gene encoding the 65-kDa heat shock protein (hsp65)
by capillary electrophoresis (CE). By using a pair of unlabeled
primers, Tb11 and Tb12, and only one restriction enzyme, HaeIII,
we investigated a total of 52 ref. and clin. strains encompassing 12
Mycobacterium species. The electrophoretic sepn. of high-resoln.
CE required <20 min and was capable of identifying fragments as small as
12 bp. A good agreement of measurement was obsd. between the sizes of
restriction fragments resolved by CE, and the real sizes were deduced from
the sequence anal. Distinct differentiations were also well demonstrated
between some species and subspecies by an extra HaeIII digestion site.
With the advantage of the complete RFLP pattern available from CE, it
appears to be more convenient to use an electropherogram rather than
performing the cumbersome slab gel electrophoresis plus diagnostic
algorithm to identify ***Mycobacterium*** species. Beyond the agarose
and polyacrylamide gel electrophoresis, high-resoln. CE provides an
alternative for rapid identification of ***Mycobacterium*** species
that is feasible for automation and routine use without the need for
costly probes.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Capillary electrophoretic restriction fragment length polymorphism
patterns for the ***mycobacterial*** hsp65 gene
AB PCR-restriction fragment length polymorphism (RFLP) anal. is a nonprobe
method for the rapid identification of ***Mycobacterium*** species.
We demonstrate the sepn. of DNA or restriction fragments digested from the
mycobacterial gene encoding the 65-kDa heat shock protein (hsp65)
by capillary electrophoresis (CE). By using a pair of unlabeled
primers, Tb11 and Tb12, and only one restriction enzyme, HaeIII,
we investigated a total of 52 ref. and clin. strains encompassing 12
Mycobacterium species. The electrophoretic sepn. of high-resoln.
CE required <20 min and was capable of identifying fragments as small as
12. . . be more convenient to use an electropherogram rather than
performing the cumbersome slab gel electrophoresis plus diagnostic
algorithm to identify ***Mycobacterium*** species. Beyond the agarose
and polyacrylamide gel electrophoresis, high-resoln. CE provides an
alternative for rapid identification of ***Mycobacterium*** species

that is feasible for automation and routine use without the need for costly probes.

ST RFLP capillary electrophoresis genotyping ***Mycobacterial*** hsp65 gene

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** , gene for; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** hsp65 gene)

IT PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(PCR-RFLP; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** hsp65 gene)

IT Capillary electrophoresis
Genotyping (method)
 Mycobacterium
 Mycobacterium abscessus
 Mycobacterium asiaticum
 Mycobacterium avium
 Mycobacterium chelonae chelonae
 Mycobacterium fortuitum
 Mycobacterium gastri
 Mycobacterium gordonaeeae
 Mycobacterium intracellulare
 Mycobacterium kansasii
 Mycobacterium phlei
 Mycobacterium smegmatis
 Mycobacterium tuberculosis
(capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** hsp65 gene)

IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(for heat shock protein hsp65; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** hsp65 gene)

IT Human
(human infection; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** hsp65 gene)

IT 81295-18-3
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** hsp65 gene)

L8 ANSWER 27 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:121485 CAPLUS <>LOGINID::20090924>>
DN 140:298231
TI Development of a single-tube, cell lysis-based, genus-specific PCR method for rapid identification of ***mycobacteria*** : optimization of cell lysis, PCR ***primers*** and conditions, and restriction pattern analysis
AU Khan, Izhar U. H.; Yadav, Jagjit S.
CS Molecular Toxicology Division, Department of Environmental Health,
University of Cincinnati Medical Center, Cincinnati, OH, 45267-0056, USA
SO Journal of Clinical Microbiology (2004), 42(1), 453-457
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology

DT Journal
LA English
AB A single-tube PCR method was developed for efficient identification of nontuberculous ***mycobacteria*** (NTM) and their environmental isolates in about 3 h without conventional DNA isolation. The following three steps were optimized or developed: (i) a simple, 6-min direct cell lysis protocol as a PCR prestep for generation of DNA-template; (ii) an improved ***Mycobacterium*** -specific PCR amplification protocol with a broader species specificity using newly designed ***primers*** targeting a 228-bp region of the 65-kDa heat shock protein (hsp) gene and optimal PCR amplification conditions; and (iii) a genus-specific restriction anal. of the PCR product for conclusive identification of the unknown NTM isolates.

OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Development of a single-tube, cell lysis-based, genus-specific PCR method for rapid identification of ***mycobacteria*** : optimization of cell lysis, PCR ***primers*** and conditions, and restriction pattern analysis

AB A single-tube PCR method was developed for efficient identification of nontuberculous ***mycobacteria*** (NTM) and their environmental isolates in about 3 h without conventional DNA isolation. The following three steps were optimized or. . . developed: (i) a simple, 6-min direct cell lysis protocol as a PCR prestep for generation of DNA-template; (ii) an improved ***Mycobacterium*** -specific PCR amplification protocol with a broader species specificity using newly designed ***primers*** targeting a 228-bp region of the 65-kDa heat shock protein (hsp) gene and optimal PCR amplification conditions; and (iii) a. . .

ST DNA sequence gene hsp ***Mycobacterium*** isolate MJY3; protein HSP65 sequence ***Mycobacterium*** isolate MJY3; gene hsp specific PCR restriction analysis identification nontuberculous ***mycobacteria***
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; use of gene hsp genus-specific PCR method followed by restriction anal. in rapid identification of nontuberculous ***mycobacteria***)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** ***65*** ; partial amino acid sequence of 65-kDa heat shock protein from ***Mycobacterium*** strain M-JY3)

IT PCR (polymerase chain reaction)
(development and optimization of single-tube cell lysis-based gene hsp genus-specific PCR method for rapid identification of nontuberculous ***mycobacteria***)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hsp; development and optimization of single-tube cell lysis-based gene hsp genus-specific PCR method for rapid identification of nontuberculous ***mycobacteria***)

IT DNA sequences
(partial DNA sequence of 65-kDa heat shock protein gene hsp amplified

from ***Mycobacterium*** strain M-JY3 using developed
 genus-specific PCR)
 IT Protein sequences
 (partial amino acid sequence of 65-kDa heat shock protein from
 Mycobacterium strain M-JY3)
 IT DNA
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***primer*** ; use of gene hsp genus-specific PCR method followed
 by restriction anal. in rapid identification of nontuberculous
 mycobacteria)
 IT ***Mycobacterium***
 (use of gene hsp genus-specific PCR method followed by restriction
 anal. in rapid identification of nontuberculous ***mycobacteria***)
 IT 638110-92-6
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; partial amino acid sequence of 65-kDa heat shock
 protein from ***Mycobacterium*** strain M-JY3)
 IT 676577-44-9 676577-45-0 676577-46-1 676577-47-2
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (gene hsp-specific ***primer*** ; use of gene hsp genus-specific PCR
 method followed by restriction anal. in rapid identification of
 nontuberculous ***mycobacteria***)
 IT 638110-91-5
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic
 use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
 USES (Uses)
 (nucleotide sequence; partial DNA sequence of 65-kDa heat shock protein
 gene hsp amplified from ***Mycobacterium*** strain M-JY3 using
 developed genus-specific PCR)

L8 ANSWER 28 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2003:591378 CAPLUS <>LOGINID::20090924>>

DN 139:146183

TI ***Primers*** for amplifying ***mycobacterial*** heat shock
 protein ***HSP*** ***65*** gene and use for identifying
 mycobacterial species

IN Kim, Bum-joon; Kook, Yoon-ho; Kim, Jeong-mi

PA Biomedlab Corporation, S. Korea

SO PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			

RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG		
KR 2003063935	A 20030731	KR 2002-4297	20020124
KR 2003072087	A 20030913	KR 2002-11648	20020305
US 20050014157	A1 20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A 20020124	
	KR 2002-11648	A 20020305	
	WO 2003-KR131	W 20030121	

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB The present invention relates to a pair of ***primers*** specific to ***mycobacterial*** species, a polynucleotide of an ***HSP*** ***65*** gene fragment, and a method for the identification of ***mycobacterial*** species by using the same. More specifically, the 604-bp ***HSP*** ***65*** gene fragment can be applied to identification methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the ***mycobacterial*** species can be identified simply, economically, and accurately.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***Primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species

AB The present invention relates to a pair of ***primers*** specific to ***mycobacterial*** species, a polynucleotide of an ***HSP*** ***65*** gene fragment, and a method for the identification of ***mycobacterial*** species by using the same. More specifically, the 604-bp ***HSP*** ***65*** gene fragment can be applied to identification methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the ***mycobacterial*** species can be identified simply, economically, and accurately.

ST ***primer*** ***mycobacteria*** heat shock protein hsp65 gene

IT Nucleic acid amplification (method)
(DNA; ***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)

IT Heat-shock proteins

RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)

(***HSP*** ***65*** ; ***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)

IT Gene, microbial

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(***HSP*** ***65*** ; ***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)

IT Diagnosis

(mol.; ***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)

IT DNA sequences

Mycobacterium	
Mycobacterium	BCG
Mycobacterium	abscessus
Mycobacterium	africanum
Mycobacterium	aichiense
Mycobacterium	asiaticum
Mycobacterium	avium
Mycobacterium	avium paratuberculosis
Mycobacterium	bovis
Mycobacterium	celatum
Mycobacterium	chelonae
Mycobacterium	chitae
Mycobacterium	farcinogenes
Mycobacterium	flavescens
Mycobacterium	fortuitum
Mycobacterium	gastri
Mycobacterium	genavense
Mycobacterium	gordonae
Mycobacterium	haemophilum
Mycobacterium	interjectum
Mycobacterium	intracellulare
Mycobacterium	kansasii
Mycobacterium	leprae
Mycobacterium	malmoense
Mycobacterium	marinum
Mycobacterium	microti
Mycobacterium	mucogenicum
Mycobacterium	neoaurum
Mycobacterium	nonchromogenicum
Mycobacterium	parafortuitum
Mycobacterium	peregrinum
Mycobacterium	phlei
Mycobacterium	scrofulaceum
Mycobacterium	senegalense
Mycobacterium	shimoidei
Mycobacterium	simiae
Mycobacterium	smegmatis
Mycobacterium	szulgai
Mycobacterium	terrae
Mycobacterium	thermoresistibile
Mycobacterium	triviale
Mycobacterium	tuberculosis
Mycobacterium	ulcerans
Mycobacterium	vaccae
Mycobacterium	wolinskyi

Nocardia carnea

RFLP (restriction fragment length polymorphism)
 Tsukamurella paurometabola
 Tsukamurella pulmonis
 Tsukamurella tyrosinosolvens
 (***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)
 IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)
 IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
 569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
 569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
 569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
 569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
 569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
 569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
 569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
 569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
 569432-52-6 569432-53-7 569432-54-8 569432-55-9
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (nucleotide sequence; ***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)
 IT 569432-56-0
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** HSPF3 sequence; ***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)
 IT 569432-57-1
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** HSPR3 sequence; ***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)
 IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)
 IT 569477-29-8
 RL: PRP (Properties)
 (unclaimed sequence; ***primers*** for amplifying ***mycobacterial*** heat shock protein ***HSP*** ***65*** gene and use for identifying ***mycobacterial*** species)

L8 ANSWER 29 OF 42 MEDLINE on STN
AN 2003395853 MEDLINE <>LOGINID::20090924>>
DN PubMed ID: 12933831
TI A DNA prime- ***Mycobacterium*** bovis BCG boost vaccination strategy for cattle induces protection against bovine tuberculosis.
AU Skinner Margot A; Buddle Bryce M; Wedlock D Neil; Keen Denise; de Lisle Geoffrey W; Tascon Ricardo E; Ferraz Jose Candido; Lowrie Douglas B; Cockle Paul J; Vordermeier H Martin; Hewinson R Glyn
CS AgResearch, Wallaceville Animal Research Centre, Upper Hutt, New Zealand..
margot.skinner@agresearch.co.nz
SO Infection and immunity, (2003 Sep) Vol. 71, No. 9, pp. 4901-7.
Journal code: 0246127. ISSN: 0019-9567.
Report No.: NLM-PMC187316.
CY United States
DT (IN VITRO)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200309
ED Entered STN: 23 Aug 2003
Last Updated on STN: 30 Sep 2003
Entered Medline: 29 Sep 2003
AB The variable efficacy of bacillus Calmette-Guerin (***Mycobacterium*** bovis BCG) in protecting humans and cattle against tuberculosis has prompted a search for a more effective vaccination regimen. A prime-boost strategy was investigated in cattle naturally sensitized to environmental ***mycobacteria*** by using a combination of three DNA vaccines coding for ***Hsp*** ***65***, Hsp 70, and Apa for priming, followed by a boost with BCG prior to experimental challenge with virulent *M. bovis*. Controls were vaccinated with DNA or BCG alone or were not vaccinated. The immune responses were monitored throughout the study, and protection was assessed based on reductions in the numbers of lesions and viable ***mycobacteria*** in lymph node samples. Vaccination with BCG alone or with a DNA prime-BCG boost regimen induced high levels of antigen-specific gamma interferon (IFN-gamma) in whole-blood cultures. In the prime-boost group there were fewer animals with severe lung lesions, fewer lymph nodes with lesions per animal, a smaller proportion of animals with lesions, lower mean lung and lymph node lesion scores, and less *M. bovis* isolated from retropharyngeal and thoracic lymph nodes compared to the results obtained for the nonvaccinated animals. The prime-boost regimen induced significant enhancement of protection in six parameters, compared with significant enhancement of protection in only two parameters for BCG alone. In addition, following challenge, in vitro IFN-gamma responses against ESAT-6 and CFP-10, as well as bovine tuberculin-induced skin test and in vitro IFN-gamma responses, were identified as immunological markers that predicted protection. The use of the prime-boost strategy suggested that a combination of vaccines may be better than a single vaccine for protection against tuberculosis.
TI A DNA prime- ***Mycobacterium*** bovis BCG boost vaccination strategy for cattle induces protection against bovine tuberculosis.
AB The variable efficacy of bacillus Calmette-Guerin (***Mycobacterium*** bovis BCG) in protecting humans and cattle against tuberculosis has prompted a search for a more effective vaccination regimen. A prime-boost strategy was investigated in cattle naturally sensitized to environmental ***mycobacteria*** by using a combination of three DNA vaccines coding

for ***Hsp*** ***65*** , Hsp 70, and Apa for priming, followed by a boost with BCG prior to experimental challenge with virulent M. bovis.. . responses were monitored throughout the study, and protection was assessed based on reductions in the numbers of lesions and viable ***mycobacteria*** in lymph node samples. Vaccination with BCG alone or with a DNA prime-BCG boost regimen induced high levels of antigen-specific. . .

CT . . . Tags: Female
Animals
*BCG Vaccine: AD, administration & dosage
BCG Vaccine: GE, genetics
Base Sequence
Birds
Cattle
Colony Count, Microbial
*** DNA Primers: GE, genetics***
Humans
Immunization, Secondary
Interferon-gamma: BI, biosynthesis
Interleukin-2: BI, biosynthesis
*** Mycobacterium bovis: GE, genetics***
*** Mycobacterium bovis: IM, immunology***
*** Mycobacterium bovis: IP, isolation & purification***
T-Lymphocytes: IM, immunology
Tuberculin: PD, pharmacology
Tuberculosis, Bovine: IM, immunology
Tuberculosis, Bovine: MI, microbiology

CN 0 (BCG Vaccine); 0 (DNA ***Primers***); 0 (Interleukin-2); 0 (Tuberculin); 0 (Vaccines, DNA)

L8 ANSWER 30 OF 42 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 1

AN 2003:181045 BIOSIS <>LOGINID::20090924>>

DN PREV200300181045

TI Development of a new sensitive and efficient multiplex polymerase chain reaction (PCR) for identification and differentiation of different ***mycobacterial*** species.

AU Bhattacharya, Basudev [Reprint Author]; Karak, Kalpana; Ghosal, Alok Gopal; Roy, Atanu; Das, Shyamal; Dandapat, Premanshu; Khetawat, Dimple; Mondal, Dibya Kanti; Bhattacharya, Sujit; Chakrabarti, Sekhar

CS Department of Biochemistry, University College of Medicine, Dr B.C. Roy Post Graduate Institute of Basic Medical Sciences, 244B Acharya J.C. Bose Road, Kolkata, 700 020, India
bbasudev@rediffmail.com

SO Tropical Medicine & International Health, (February 2003) Vol. 8, No. 2, pp. 150-157. print.
ISSN: 1360-2276.

DT Article

LA English

ED Entered STN: 9 Apr 2003
Last Updated on STN: 9 Apr 2003

AB For early detection and species differentiation of ***mycobacteria*** , polymerase chain reaction (PCR) techniques are currently in wide use. However, individual techniques using amplification of different targets with appropriate ***primers*** still have some limitations, which have

to be overcome. The ideal technique would use DNA sequences which should be present in all ***mycobacteria*** and absent in others and would be able to discriminate one species from the other, as non-tuberculous ***mycobacteria*** (NTM) are on rise in terms of frequency of detection.

We developed a multiplex PCR based on amplification of 165, 365 and 541 bp target fragments of unrelated genes, ***hsp*** ***65*** coding for 65 kDa antigen, dnaJ gene of ***mycobacteria*** and insertion element IS 6110 of ***Mycobacterium*** tuberculosis, respectively. This multiplex PCR was tested over 5 years from 1996 to 2001 with 411 clinical specimens from suspected cases of tuberculosis and ***mycobacterioses*** and compared with standard laboratory techniques. The multiplex PCR was positive for 379 cases compared with 280 cases by standard techniques ($P<0.0001$). It could distinguish between strains of the *M. tuberculosis* complex and NTM; the results are comparable with standard techniques. Thus the multiplex PCR can be useful in early detection, species differentiation and epidemiology.

TI Development of a new sensitive and efficient multiplex polymerase chain reaction (PCR) for identification and differentiation of different ***mycobacterial*** species.

AB For early detection and species differentiation of ***mycobacteria***, polymerase chain reaction (PCR) techniques are currently in wide use. However, individual techniques using amplification of different targets with appropriate ***primers*** still have some limitations, which have to be overcome. The ideal technique would use DNA sequences which should be present in all ***mycobacteria*** and absent in others and would be able to discriminate one species from the other, as non-tuberculous ***mycobacteria*** (NTM) are on rise in terms of frequency of detection.

We developed a multiplex PCR based on amplification of 165, 365 and 541 bp target fragments of unrelated genes, ***hsp*** ***65*** coding for 65 kDa antigen, dnaJ gene of ***mycobacteria*** and insertion element IS 6110 of ***Mycobacterium*** tuberculosis, respectively. This multiplex PCR was tested over 5 years from 1996 to 2001 with 411 clinical specimens from suspected cases of tuberculosis and ***mycobacterioses*** and compared with standard laboratory techniques. The multiplex PCR was positive for 379 cases compared with 280 cases by standard. . .

ORGN Classifier

Mycobacteriaceae 08881

Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms;

Eubacteria; Bacteria; Microorganisms

Organism Name

Mycobacterium avium (species): pathogen, clinical isolates

Mycobacterium bovis (species): pathogen, clinical isolates

Mycobacterium intracellulare (species): pathogen, clinical isolates

Mycobacterium smegmatis (species): pathogen, clinical isolates

Mycobacterium tuberculosis (species): pathogen, clinical isolates

non-tuberculous ***mycobacteria*** (common): pathogen, clinical isolates

Taxa Notes

Bacteria, Eubacteria, Microorganisms

GEN ***mycobacteria*** dnaJ gene (***Mycobacteriaceae***);
mycobacteria ***hsp*** ***65*** gene (

Mycobacteriaceae)

L8 ANSWER 31 OF 42 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN
AN 2003:528770 BIOSIS <>LOGINID::20090924>>
DN PREV200300524583
TI EVALUATION OF GENOTYPIC AND PHENOTYPIC IDENTIFICATION METHODS FOR
SPECIATION OF OCULAR ISOLATES OF ***MYCOBACTERIA*** .
AU Therese, K. L. [Reprint Author]; Madhavan, J. Therese P. Deepa R.
Pusphalatha H. N.
CS Microbiology Research Centre, Vision Research Foundation 18 College Road,
Chennai, India
SO ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003,
pp. Abstract No. 1427. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision
and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association
for Research in Vision and Ophthalmology.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 12 Nov 2003
Last Updated on STN: 12 Nov 2003
AB Purpose: To identify the ocular ***mycobacterial*** isolates to
species level rapidly by Polymerase chain reaction based Restriction
Fragment Length Polymorphism (PCR-RFLP) technique using three sets of
primers coding for two different genes of ***mycobacteria***
and to evaluate the techniques with the conventional standard biochemical
tests . Methods: :Eighteen ocular ***mycobacterial*** isolates (7
corneal scrapings, 4 Fine needle aspiration biopsy (FNAB) from sub retinal
mass, 2 cannalicular pus , 1 scleral iris mass , 3 intraocular fluids, and
1 intraocular lens(IOL) from 14 patients were included in the study.
PCR-RFLP technique using three sets of ***primers*** (setI-coding for
16-23 ribosomal DNA interspacer sequences Sets II & III-coding for
****HSP*** ****65*** gene) were standardised for specificity and
sensitivity and applied on all 18 isolates of ***mycobacteria*** .The
amplified products of were digested with restriction enzymes,Hae III,Msp I
and Bst XI , ***primer*** set I Xho I and Bst NI with ***Primer***
set II, and Hae III, and Bst E11 with ***primer*** set III.The
identification of the ***mycobacterial*** isolates were carried out by
conventional biochemical tests, including substrate utilization tests.
Results: The ***primer*** set I could differentiate the 18 isolates
into 7 slow growers (325-370 bp) and 11 rapid growers (420-520 bp)of
mycobacteria . The ***primer*** set II and III resulted in
1380 bp and 439 bp amplified products respectively for all
mycobacterial isolates. Further based on the RFLP pattern all
the
7 slow growers (4 FNAB from sub retinal mass,1 corneal scraping 1 scleral
iris mass, 1 cannalicular pus) were identified as ***Mycobacterium***
tuberculosis and among the 11 rapid growers 10 were identified as
Mycobacterium chelonae and 1 as ***Mycobacterium*** fortuitum
Conclusions: To identify ocular ***mycobacterial*** isolates to
species level, the conventional biochemical techniques required minimum 3
weeks for rapid growers, and 4 weeks for slow growers whereas the PCR-RFLP
techniques required only 8-10 hours time.Among the 3 PCR-RFLP techniques
the ***primer*** set III coding for 65KD gene was considered as the
most suitable technique for rapid and accurate identification of
mycobacteria to species level.

TI EVALUATION OF GENOTYPIC AND PHENOTYPIC IDENTIFICATION METHODS FOR
SPECIATION OF OCULAR ISOLATES OF ***MYCOBACTERIA*** .

AB Purpose: To identify the ocular ***mycobacterial*** isolates to species level rapidly by Polymerase chain reaction based Restriction Fragment Length Polymorphism (PCR-RFLP) technique using three sets of ***primers*** coding for two different genes of ***mycobacteria*** and to evaluate the techniques with the conventional standard biochemical tests . Methods: Eighteen ocular ***mycobacterial*** isolates (7 corneal scrapings, 4 Fine needle aspiration biopsy (FNAB) from sub retinal mass, 2 cannalicular pus , 1 scleral. . . intraocular fluids, and 1 intraocular lens(IOL) from 14 patients were included in the study. PCR-RFLP technique using three sets of ***primers*** (setI-coding for 16-23 ribosomal DNA interspacers sequences Sets II & III-coding for ***HSP*** ***65*** gene) were standardised for specificity and sensitivity and applied on all 18 isolates of ***mycobacteria*** .The amplified products of were digested with restriction enzymes,Hae III,Msp I and Bst XI , ***primer*** set I Xho I and Bst NI with ***Primer*** set II, and Hae III, and Bst E11 with ***primer*** set III.The identification of the ***mycobacterial*** isolates were carried out by conventional biochemical tests, including substrate utilization tests. Results: The ***primer*** set I could differentiate the 18 isolates into 7 slow growers (325-370 bp) and 11 rapid growers (420-520 bp)of ***mycobacteria*** . The ***primer*** set II and III resulted in 1380 bp and 439 bp amplified products respectively for all ***mycobacterial*** isolates. Further based on the RFLP pattern all the 7 slow growers (4 FNAB from sub retinal mass,1 corneal scraping 1 scleral iris mass, 1 cannalicular pus) were identified as ***Mycobacterium*** tuberculosis and among the 11 rapid growers 10 were identified as ***Mycobacterium*** chelonae and 1 as ***Mycobacterium*** fortuitum Conclusions: To identify ocular ***mycobacterial*** isolates to species level, the conventional biochemical techniques required minimum 3 weeks for rapid growers, and 4 weeks for slow growers whereas the PCR-RFLP techniques required only 8-10 hours time.Among the 3 PCR-RFLP techniques the ***primer*** set III coding for 65KD gene was considered as the most suitable technique for rapid and accurate identification of ***mycobacteria*** to species level.

ORGN Classifier
 Mycobacteriaceae 08881

Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms

Organism Name
 mycobacteria (genus)

Taxa Notes
 Bacteria, Eubacteria, Microorganisms

L8 ANSWER 32 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:932193 CAPLUS <<LOGINID::20090924>>
DN 142:87549
TI Drug sensitivity test method for ***Mycobacterium*** leprae using reverse transcription-polymerase chain reaction (RT-PCR)
IN Kim, Min Ju; Kim, Sang Heon; Kim, Se Gon; You, Ji Chang
PA S. Korea
SO Repub. Korean Kongkae Taeho Kongbo, No pp. given
CODEN: KRXXA7
DT Patent

LA Korean

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 2001094219	A	20011031	KR 2000-17727	20000404
PRAI	KR 2000-17727			20000404	

- AB Provided is a drug sensitivity test method for ***Mycobacterium*** leprae (hereafter referred to as M.leprae), using reverse transcription polymerase chain reaction(RT-PCR), thereby assaying drug efficacy in a simple, fast, reliable, accurate and sensible manner compared with other existing tests which need costly equipment. The method can be used in developing therapeutic agents in Hansen's disease and deciding the effectiveness of chemotherapeutic treatment in Hansen's disease. The test method comprises steps of: (i) infecting M.leprae to a host cell in a ratio of cell no. to M.leprae no. being 1:10 to 1:30, for 8 h, where the host cell is characteristically mouse macrophage cell line IC-21, J77rA.1, RAW 264.17 or THP-1 and treating an antibiotics for Hansen's disease for 12 to 24 h to test sensitivity, where antibiotics is selected from rifampin, Dapsone (4,4-diamino di-Ph sulfone), clofazimine, mimocin, ethonamide, fluoroquinolones, macrolide antibiotics, minocycline and fusidic acid; (ii) sepg. M.leprae from the host cell, extg. RNA from sepd. M.leprea and obtaining cDNA by reverse transcription from the extd. RNA as a template; (iii) amplifying the obtained cDNA by polymerase chain reaction(PCR) using M.leprae-specific 18kDa gene ***primer*** 1(SEQ NO ID:1) and 2(SEQ ID NO:2) and the reaction target base sequence selected from the group consisting of the heat shock protein, hsp 10, 14, 34, 45, 65 or 70 gene, Dmak gene, GroEl gene, 16S rRNA, 16S rRNA, M.leprae-specific 18kDa gene, and M.leprae specific repetitive sequence and finally performing agarose gel electrophoresis.
- TI Drug sensitivity test method for ***Mycobacterium*** leprae using reverse transcription-polymerase chain reaction (RT-PCR)
- AB Provided is a drug sensitivity test method for ***Mycobacterium*** leprae (hereafter referred to as M.leprae), using reverse transcription polymerase chain reaction(RT-PCR), thereby assaying drug efficacy in a simple, fast, . . . from the extd. RNA as a template; (iii) amplifying the obtained cDNA by polymerase chain reaction(PCR) using M.leprae-specific 18kDa gene ***primer*** 1(SEQ NO ID:1) and 2(SEQ ID NO:2) and the reaction target base sequence selected from the group consisting of the . . .
- ST ***Mycobacterium*** drug sensitivity test PCR ***primer***
- IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S, gene; drug sensitivity test method for ***Mycobacterium*** leprae using reverse transcription-polymerase chain reaction (RT-PCR))
- IT Gene, microbial
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(16S rRNA; drug sensitivity test method for ***Mycobacterium*** leprae using reverse transcription-polymerase chain reaction (RT-PCR))
- IT Gene, microbial
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(Dmak; drug sensitivity test method for ***Mycobacterium*** leprae using reverse transcription-polymerase chain reaction (RT-PCR))
- IT Heat-shock proteins
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(***HSP*** ***65*** ; drug sensitivity test method for
Mycobacterium leprae using reverse transcription-polymerase
chain reaction (RT-PCR))

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(HSP 70; drug sensitivity test method for ***Mycobacterium***
leprae using reverse transcription-polymerase chain reaction (RT-PCR))

IT PCR (polymerase chain reaction)
(RT-PCR (reverse transcription-PCR); drug sensitivity test method for
Mycobacterium leprae using reverse transcription-polymerase
chain reaction (RT-PCR))

IT Antibacterial agents
Drug screening
Drugs
Leprosy
Macrophage
Mus musculus
Mycobacterium leprae
(drug sensitivity test method for ***Mycobacterium*** leprae using
reverse transcription-polymerase chain reaction (RT-PCR))

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(drug sensitivity test method for ***Mycobacterium*** leprae using
reverse transcription-polymerase chain reaction (RT-PCR))

IT Gene, microbial
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(groEL; drug sensitivity test method for ***Mycobacterium*** leprae
using reverse transcription-polymerase chain reaction (RT-PCR))

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(hsp 10, 14, 34, 45; drug sensitivity test method for
Mycobacterium leprae using reverse transcription-polymerase
chain reaction (RT-PCR))

IT Antibiotics
(macrolide; drug sensitivity test method for ***Mycobacterium***
leprae using reverse transcription-polymerase chain reaction (RT-PCR))

IT 60-35-5, Ethanamide, biological studies 80-08-0, Dapsone 2030-63-9,
Clofazimine 6990-06-3, Fusidic acid 10118-90-8, Minocycline
13292-46-1, Rifampin 76177-28-1, Mimocin
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(drug sensitivity test method for ***Mycobacterium*** leprae using
reverse transcription-polymerase chain reaction (RT-PCR))

L8 ANSWER 33 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:647495 CAPLUS <>LOGINID::20090924>>
DN 136:304792
TI Identification of 54 ***mycobacterial*** species by PCR-restriction
fragment length polymorphism analysis of the hsp65 gene
AU Brunello, Francesca; Ligozzi, Marco; Cristelli, Emanuela; Bonora, Stefano;
Tortoli, Enrico; Fontana, Roberta
CS Dipartimento di Patologia, Sezione di Microbiologia, Universita di Verona
and Servizio di Microbiologia dell'Azienda Ospedaliera di Verona, Verona,

37100, Italy
SO Journal of Clinical Microbiology (2001), 39(8), 2799-2806
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB A total of 121 ref. and clin. strains of both slowly and rapidly growing ***mycobacteria*** belonging to 54 species were studied for restriction fragment length polymorphism of a PCR-amplified 439-bp segment of the gene encoding the 65-kDa heat shock protein. Restriction digests were sep'd. by 10% polyacrylamide gel electrophoresis (PAGE). By including a size std. in each sample, the restriction fragment profile was calcd. using a computer-aided comparison program. An algorithm describing these 54 species (including 22 species not previously described) is proposed. We found that this assay based on 10% PAGE provided a more precise est. than that based on agarose gel electrophoresis of the real size of restriction fragments as deduced from the sequence anal. and allowed identification of ***mycobacteria*** whose PCR-restriction fragment length polymorphism anal. patterns were unequivocally identified by fragments shorter than 60 bp.
OSC.G 47 THERE ARE 47 CAPLUS RECORDS THAT CITE THIS RECORD (47 CITINGS)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Identification of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism analysis of the hsp65 gene
AB A total of 121 ref. and clin. strains of both slowly and rapidly growing ***mycobacteria*** belonging to 54 species were studied for restriction fragment length polymorphism of a PCR-amplified 439-bp segment of the gene encoding. . . agarose gel electrophoresis of the real size of restriction fragments as deduced from the sequence anal. and allowed identification of ***mycobacteria*** whose PCR-restriction fragment length polymorphism anal. patterns were unequivocally identified by fragments shorter than 60 bp.
ST DNA sequence ***Mycobacterium*** gene hsp65 protein; genotyping PCR RFLP polyacrylamide gel electrophoresis algorithm ***Mycobacterium*** hsp65
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; identification of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the hsp65 gene)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** ***65*** ; identification of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the hsp65 gene)
IT RFLP (restriction fragment length polymorphism)
(PCR-; identification of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the hsp65 gene)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene hsp65; identification of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the hsp65 gene)
IT Algorithm
Gel electrophoresis

Genotyping (method)

Mycobacterium	abscessus
Mycobacterium	agri
Mycobacterium	aichiense
Mycobacterium	alvei
Mycobacterium	asiaticum
Mycobacterium	austroafricanum
Mycobacterium	avium
Mycobacterium	avium paratuberculosis
Mycobacterium	branderi
Mycobacterium	brumae
Mycobacterium	celatum
Mycobacterium	chelonae
Mycobacterium	chitae
Mycobacterium	confluentis
Mycobacterium	duvalii
Mycobacterium	fallax
Mycobacterium	farcinogenes
Mycobacterium	fortuitum
Mycobacterium	gadium
Mycobacterium	gastri
Mycobacterium	genavense
Mycobacterium	gilvum
Mycobacterium	gordonae
Mycobacterium	haemophilum
Mycobacterium	hiberniae
Mycobacterium	interjectum
Mycobacterium	intracellulare
Mycobacterium	kansasii
Mycobacterium	malmense
Mycobacterium	marinum
Mycobacterium	mucogenicum
Mycobacterium	neoaurum
Mycobacterium	nonchromogenicum
Mycobacterium	obuense
Mycobacterium	peregrinum
Mycobacterium	phlei
Mycobacterium	porcinum
Mycobacterium	poriferae
Mycobacterium	pulveris
Mycobacterium	rhodesiae
Mycobacterium	scrofulaceum
Mycobacterium	senegalense
Mycobacterium	shimoidei
Mycobacterium	siernhoferi
Mycobacterium	simiae
Mycobacterium	smegmatis
Mycobacterium	szulgai

PCR (polymerase chain reaction)

(identification of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the hsp65 gene)

IT Protein sequences

(of gene hsp65 heat shock protein isolated from ***Mycobacterium*** species)

IT DNA sequences

(of gene hsp65 isolated from ***Mycobacterium*** species)

IT DNA

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** ; identification of 54 ***mycobacterial*** species
 by PCR-restriction fragment length polymorphism anal. of the hsp65
 gene)

IT	409133-45-5	409133-46-6	409133-47-7	409133-48-8	409133-49-9
	409133-50-2	409133-51-3	409133-52-4	409133-53-5	409133-54-6
	409133-55-7	409133-56-8	409133-57-9	409133-58-0	409133-59-1
	409133-60-4	409133-61-5	409133-62-6	409133-63-7	409133-64-8
	409133-65-9	409133-66-0	409133-67-1	409133-68-2	409133-69-3
	409133-70-6	409133-71-7	409133-72-8	409133-73-9	409133-74-0
	409133-75-1	409133-76-2	409133-77-3	409133-78-4	409133-79-5
	409133-80-8	409133-81-9	409133-82-0	409400-81-3	409400-82-4
	409400-83-5	409400-84-6	409400-85-7	409400-86-8	409400-87-9
	409400-88-0				

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; identification of 54 ***mycobacterial*** species
 by PCR-restriction fragment length polymorphism anal. of the
 hsp65 gene)

IT	81295-18-3	93229-61-9, Restriction endonuclease BstEII			
		RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)			
		(identification of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the hsp65 gene)			

IT	330543-09-4, GenBank AJ310216	330543-10-7, GenBank AJ310217			
	330543-11-8, GenBank AJ310218	330543-12-9, GenBank AJ310219			
	330543-13-0, GenBank AJ310221	330543-14-1, GenBank AJ310223			
	330543-15-2, GenBank AJ310225	330543-16-3, GenBank AJ310226			
	330543-17-4, GenBank AJ310229	330543-18-5, GenBank AJ310230			
	330543-19-6, GenBank AJ310231	330543-20-9, GenBank AJ310232			
	330543-21-0, GenBank AJ310233	330543-22-1, GenBank AJ310236			
	330543-23-2, GenBank AJ310238	330777-51-0, GenBank AJ307630			
	330777-52-1, GenBank AJ307631	330777-53-2, GenBank AJ307632			
	330777-54-3, GenBank AJ307636	330777-55-4, GenBank AJ307640			
	330777-56-5, GenBank AJ307641	330777-57-6, GenBank AJ307643			
	330777-58-7, GenBank AJ307644	330777-59-8, GenBank AJ307645			
	330777-60-1, GenBank AJ307646	330777-61-2, GenBank AJ307647			
	330777-62-3, GenBank AJ307651	330777-63-4, GenBank AJ307652			
	330777-64-5, GenBank AJ307654	383716-71-0, GenBank AJ310215			
	383716-72-1, GenBank AJ310224	383716-73-2, GenBank AJ310228			
	383716-75-4, GenBank AJ310237	383716-76-5, GenBank AJ307637			
	383716-77-6, GenBank AJ307649	383716-78-7, GenBank AJ307653			
	384598-59-8, GenBank AJ310220	384598-71-4, GenBank AJ310234			
	384598-73-6, GenBank AJ310235	384598-75-8, GenBank AJ310239			
	384598-89-4, GenBank AJ307634	384598-91-8, GenBank AJ307635			
	384598-93-0, GenBank AJ307638	384598-95-2, GenBank AJ307639			
	384598-97-4, GenBank AJ307648	384598-99-6, GenBank AJ307650			
	385635-00-7, GenBank AJ310227	385635-02-9, GenBank AJ307642			
	385652-99-3, GenBank AJ310222	385653-01-0, GenBank AJ307633			

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide sequence; identification of 54 ***mycobacterial*** species
 by PCR-restriction fragment length polymorphism anal. of the
 hsp65 gene)

AN 1999:595536 CAPLUS <<LOGINID::20090924>>
DN 132:118005
TI Determination of the sensitivity and specificity of PCR assays using different target DNAs for the detection of ***Mycobacterium*** tuberculosis
AU Wei, Cheng-Yu; Lee, Chun N.; Chu, Chin-Hwa; Hwang, Jiuan Jiuan; Lee, Chan Ping
CS Tzu Chi College of Medicine and Humanities, Tzu Chi General Hospital, Hualien, Taiwan
SO Kaohsiung Journal of Medical Sciences (1999), 15(7), 396-405
CODEN: KJMSFM; ISSN: 0257-5655
PB Kaohsiung Journal of Medical Sciences
DT Journal
LA English
AB To establish a sensitive, specific and reproducible PCR assay for the detection of ***Mycobacterium*** tuberculosis, we evaluated three target DNAs: IS6110, 65 kDa heat shock protein gene; and mtp40 genomic fragment. We purified genomic DNA from 15 ***mycobacterial*** strains including four M. tuberculosis isolates, four M. bovis BCG isolates, and one of each for M. fortuitum, M. avium, M. intracellulare, M. szulgai, M. scrofulaceum, M. chelonei, and M. gordonae from the culture and used them as the template DNA. We studied 3 ***primer*** sets for IS6110, 2 ***primer*** sets for 65 kDa heat shock protein gene, and 3 ***primer*** sets for mtp40. Depending on the assay, these ***primer*** sets were used in the single-step PCR and/or nested PCR. The PCR assay targeting the 65 kDa protein gene could detect all of the tested ***mycobacterial*** strains, whereas targeting the IS6110 sequence resulted in detection of only M. tuberculosis and M. bovis BCG. Furthermore, targeting the mtp40 genomic fragment could be used to distinguish M. tuberculosis from M. bovis BCG. Using a nested PCR assay with ***primer*** sets specifically targeting the IS6110 or 65 kDa, we have been able to detect single copy M. tuberculosis genomic DNA. When the mtp40 genomic fragment was used as the target DNA, the sensitivity of detection was 10 copies of M. tuberculosis genomic DNA. This assay was demonstrated to have good sensitivity and specificity for detection and discrimination of ***mycobacterial*** species, and could be used in analyzing the clin. samples with low copy no. infections such as the cerebrospinal fluid from the patient with tuberculous meningitis.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Determination of the sensitivity and specificity of PCR assays using different target DNAs for the detection of ***Mycobacterium*** tuberculosis
AB To establish a sensitive, specific and reproducible PCR assay for the detection of ***Mycobacterium*** tuberculosis, we evaluated three target DNAs: IS6110, 65 kDa heat shock protein gene; and mtp40 genomic fragment. We purified genomic DNA from 15 ***mycobacterial*** strains including four M. tuberculosis isolates, four M. bovis BCG isolates, and one of each for M. fortuitum, M. avium, M. scrofulaceum, M. chelonei, and M. gordonae from the culture and used them as the template DNA. We studied 3 ***primer*** sets for IS6110, 2 ***primer*** sets for 65 kDa heat shock protein gene, and 3 ***primer*** sets for mtp40. Depending on the assay, these ***primer*** sets were used in the single-step PCR and/or nested PCR. The PCR assay targeting the 65 kDa protein gene could detect all of the tested ***mycobacterial*** strains, whereas targeting the IS6110 sequence resulted in detection of

only M. tuberculosis and M. bovis BCG. Furthermore, targeting the . . . mtp40 genomic fragment could be used to distinguish M. tuberculosis from M. bovis BCG. Using a nested PCR assay with ***primer*** sets specifically targeting the IS6110 or 65 kDa, we have been able to detect single copy M. tuberculosis genomic DNA. . . . of M. tuberculosis genomic DNA. This assay was demonstrated to have good sensitivity and specificity for detection and discrimination of ***mycobacterial*** species, and could be used in analyzing the clin. samples with low copy no. infections such as the cerebrospinal fluid. . . .

ST PCR ***Mycobacterium*** tuberculosis detection IS6110 mtp40 hsp65

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** , gene for; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT Insertion sequence
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(IS6110; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT ***Mycobacterium*** tuberculosis
PCR (polymerase chain reaction)
(detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT Diagnosis
(mol.; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(mtp40; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT 256216-29-2 256216-30-5 256216-31-6 256216-32-7
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(PCR ***primer*** for IS6110; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT 256216-33-8 256216-34-9 256216-35-0 256216-36-1
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(PCR ***primer*** for mtp40; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

L8 ANSWER 35 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:436334 CAPLUS <<LOGINID::20090924>>
DN 131:253056
TI Characterization to species level of clinical isolates of the

Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme analysis

AU Garriga, Xavier; Cortes, Pilar; March, Francesca; Rodriguez, Purificacion; Garrigo, Montserrat; Moreno, Carmen; Garcia, Elena; Coll, Pere; Prats, Guillem

CS Servei de Microbiologia, Hospital de la Santa Creu i Sant Pau, Barcelona, 08025, Spain

SO Clinical Microbiology and Infection (1999), 5(6), 379-382
CODEN: CMINFM; ISSN: 1198-743X

PB Decker Europe

DT Journal

LA English

AB The AccuProbe System was used to classify clin. isolates of *M. avium* and *M. intracellulare*. ***Primers*** were used to amplify specific DNA fragments (DT1-DT6) for identification of these isolates by PCR. In addn., PCR-restriction enzyme anal. (PRA) was performed on these strains based on ***primers*** amplifying a fragment of the gene hsp65. PRA was more sensitive than the AccuProbe System and DT1-DT6 amplification.

OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Characterization to species level of clinical isolates of the ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme analysis

AB The AccuProbe System was used to classify clin. isolates of *M. avium* and *M. intracellulare*. ***Primers*** were used to amplify specific DNA fragments (DT1-DT6) for identification of these isolates by PCR. In addn., PCR-restriction enzyme anal. (PRA) was performed on these strains based on ***primers*** amplifying a fragment of the gene hsp65. PRA was more sensitive than the AccuProbe System and DT1-DT6 amplification.

ST ***Mycobacterium*** diagnosis probe restriction enzyme PCR

IT Nucleic acid hybridization
(DNA-DNA; characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT Heat-shock proteins
RL: ADV (Adverse effect, including toxicity); ARU (Analytical role, unclassified); ANST (Analytical study); BIOL (Biological study)
(***HSP*** ***65*** ; characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT Diagnosis
Mycobacterium avium
Mycobacterium intracellulare
PCR (polymerase chain reaction)
(characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT Gene, microbial
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)

(hsp65; characterization to species level of clin. isolates of
Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
PCR-restriction enzyme anal.)

IT 81295-18-3 93229-61-9, Restriction endonuclease BstEII 148908-88-7,
DNA, d(C-G-T-T-C-G-A-T-C-G-C-A-G-T-T-T-G-T-G-C-A-G-C-G-C-G-T-A-C-A)
148908-89-8, DNA, d(A-T-G-G-C-C-G-G-A-G-A-C-G-A-T-C-T-A-T-G-C-C-G-G-C-G-
T-A-C) 150951-89-6 150951-90-9
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
study); BIOL (Biological study); USES (Uses)
(characterization to species level of clin. isolates of
Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
PCR-restriction enzyme anal.)

L8 ANSWER 36 OF 42 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 2

AN 2000:55199 BIOSIS <>LOGINID::20090924>>

DN PREV200000055199

TI Polymerase chain reaction-restriction fragment length polymorphism
(PCR-RFLP) analysis and plasmid profile of soil and clinical isolates of
Nocardia.

AU Qasem, J. A.; Khan, Z. U. [Reprint author]; Mustafa, A. S.; Chugh, T. D.

CS Department of Microbiology, Faculty of Medicine, Kuwait University,
Kuwait, Kuwait

SO Microbiological Research, (Sept., 1999) Vol. 154, No. 2, pp. 157-165.
print.

ISSN: 0944-5013.

DT Article

LA English

ED Entered STN: 3 Feb 2000

Last Updated on STN: 3 Jan 2002

AB The aim of this study was to develop a polymerase chain
reaction-restriction fragment length polymorphism (PCR-RFLP) assay for
generic and species-specific differentiation of Nocardia from other
morphologically similar bacterial pathogens. To examine the utility of
the PCR-RFLP approach in species identification, genomic DNA was prepared
from 40 soil isolates, 10 clinical isolates and 8 reference strains of
Nocardia. A set of oligonucleotide ***primers*** was designed from
the consensus sequence of the highly conserved groEL gene that encodes the
65-kDa heat shock protein (***hsp*** ***65***). The

primers selectively amplified 422 bp DNA from the genomic DNA of
all Nocardia species and isolates. The digestion of the amplicons with
the restriction enzyme MspI produced DNA fragments that could
differentiate between different Nocardia species regardless of their
origin. Additionally, the RFLP patterns obtained with restriction enzymes
MspI and BsaHI resulted in the differentiation of six Nocardia species
which were earlier identified by biochemical tests. Apart from soil
isolates of *N. asteroides*, which had shown some degree of genotypic
polymorphism with BsaHI, the remaining taxa yielded more consistent
results. Our results on the isolation of plasmids indicated that their
occurrence is not a consistent feature in Nocardia species. It is neither
related to the source of origin (clinical versus saprobic), nor to
virulence, antimicrobial resistance or species specificity.

AB . . . DNA was prepared from 40 soil isolates, 10 clinical isolates and 8
reference strains of Nocardia. A set of oligonucleotide ***primers***
was designed from the consensus sequence of the highly conserved groEL
gene that encodes the 65-kDa heat shock protein (***hsp*** ***65***
). The ***primers*** selectively amplified 422 bp DNA from the

genomic DNA of all Nocardia species and isolates. The digestion of the amplicons. . .

IT . . .
and Techniques

IT Chemicals & Biochemicals
BsaHI: reagent, restriction enzyme; DNA: genomic; MspI: reagent,
restriction enzyme; heat shock protein 65 [***hsp*** ***65***];
Mycobacterium tuberculosis groEL gene

L8 ANSWER 37 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:200588 CAPLUS <>LOGINID::20090924>>
DN 131:68708

TI Polymerase chain reaction, with sequencing, as a diagnostic tool in culture-negative bacterial meningitis

AU Dicuonzo, Giordano; Lorino, Giulia; Lilli, Daniela; Rivanera, Daniela; Guarino, Paola; Angeletti, Silvia; Gherardi, Giovanni; Filadoro, Francesco

CS Libera Universita, Campus Bio-Medico, Facolta Medicina e Chirurgia, Universita "La Sapienza", Rome, 00155, Italy

SO Clinical Microbiology and Infection (1999), 5(2), 92-96
CODEN: CMINFM; ISSN: 1198-743X

PB Decker Europe

DT Journal

LA English

AB To evaluate the feasibility of using 16S rDNA universal ***primer*** PCR (followed by sequencing) and 65-kDa heat shock ***Mycobacterium*** tuberculosis protein gene PCR as a method to det. a bacterial etiol. in culture-neg. cerebrospinal fluid (CSF) samples. One hundred and forty-nine CSF samples from 128 patients were processed. DNA was extd. from the CSF samples and amplified with the eubacterial 16S rDNA ***primers*** P11E and P13B, and with the 65-kDa heat shock protein gene ***mycobacterial*** ***primers*** . The amplicons were identified by sequencing and specific oligoprobe hybridization. Overall, a microbiol. diagnosis was made in 11 of 125 ultimately culture-neg. cases. The use of 65-kDa heat shock protein gene PCR was needed to improve the diagnosis of tuberculous meningitis; in four patients, prospectively studied, the outcome of antituberculous therapy could also be followed. In culture-neg. bacterial meningitis it is possible to improve the microbiol. diagnosis by use of 16S rDNA amplification and sequencing, together with amplification of a more specific gene in ***mycobacteria*** .

OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB To evaluate the feasibility of using 16S rDNA universal ***primer*** PCR (followed by sequencing) and 65-kDa heat shock ***Mycobacterium*** tuberculosis protein gene PCR as a method to det. a bacterial etiol. in culture-neg. cerebrospinal fluid (CSF) samples. One hundred. . . samples from 128 patients were processed. DNA was extd. from the CSF samples and amplified with the eubacterial 16S rDNA ***primers*** P11E and P13B, and with the 65-kDa heat shock protein gene ***mycobacterial*** ***primers*** . The amplicons were identified by sequencing and specific oligoprobe hybridization. Overall, a microbiol. diagnosis was made in 11 of 125. . . the microbiol. diagnosis by use of 16S rDNA amplification and sequencing, together with amplification of a more specific gene in ***mycobacteria*** .

IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S; PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)
IT ***Primers*** (nucleic acid)
Primers (nucleic acid)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** ; PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)
IT Gene, animal
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(HSP65; PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)
IT ***Mycobacterium*** tuberculosis
PCR (polymerase chain reaction)
(PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)
IT Diagnosis
(mol.; PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)
IT DNA
DNA
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)
IT DNA
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rDNA, 16 S; PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)
IT Meningitis
(tuberculous; PCR using 16S rDNA and HSP65 protein ***primers*** of DNA from cerebrospinal fluid in diagnosis of culture-neg. tuberculous meningitis in humans)

L8 ANSWER 38 OF 42 CABA COPYRIGHT 2009 CABI on STN
AN 2000:159044 CABA <<LOGINID::20090924>>
DN 20002220746
TI Detection and identification of ***Mycobacterium*** bovis using polymerase chain reaction (PCR)
Deteccao e identificacao de ***Mycobacterium*** bovis pela reacao em cadeia da polimerase (PCR)

AU Sakamoto, S. M.; Heinemann, M. B.; Telles, M. A. S.; Roxo, E.; Richtzenhain, L. J.; Vasconcellos, S. A.; Ferreira Neto, J. S.

CS Departamento de Medicina Veterinaria Preventiva e Saude Animal, FMVZ-USP, Av. Prof. Dr. Orlando Marques de Paiva 87, CEP 05508-900, Sao Paulo, SP, Brazil.

SO Arquivos do Instituto Biologico (Sao Paulo), (1999) Vol. 66, No. 2, pp. 45-58. 3 pp. of ref.

ISSN: 0020-3653

DT Journal

LA Portuguese

SL English

ED Entered STN: 8 Dec 2000
Last Updated on STN: 8 Dec 2000

AB Two methods of DNA extraction (alkaline lysis and proteinase-based) were compared and 3 ***primer*** pairs were evaluated. The 1st ***primer*** pair detected ***Mycobacterium*** spp. (383 bp fragment included in ***HSP*** ***65*** kD codifying gene), the 2nd detected the *M. tuberculosis* complex (419 bp fragment inside the Pab 38 kD gene), and the 3rd detected *M. bovis* (500 bp DNA fragment). The alkaline lysis method presented higher quantities of extracted DNA with more DNA degradation than the proteinase-based method. PCR carried out against pure cultures of either reference strains or clinical isolates classified all ***mycobacteria*** samples correctly.

TI [Detection and identification of ***Mycobacterium*** bovis using polymerase chain reaction (PCR)].
Deteccao e identificacao de ***Mycobacterium*** bovis pela reacao em cadeia da polimerase (PCR).

AB Two methods of DNA extraction (alkaline lysis and proteinase-based) were compared and 3 ***primer*** pairs were evaluated. The 1st ***primer*** pair detected ***Mycobacterium*** spp. (383 bp fragment included in ***HSP*** ***65*** kD codifying gene), the 2nd detected the *M. tuberculosis* complex (419 bp fragment inside the Pab 38 kD gene), and . . . degradation than the proteinase-based method. PCR carried out against pure cultures of either reference strains or clinical isolates classified all ***mycobacteria*** samples correctly.

BT ***Mycobacterium*** ; ***Mycobacteriaceae*** ; Firmicutes; bacteria; prokaryotes

ORGN ***Mycobacterium*** bovis; ***Mycobacterium*** ; ***Mycobacterium*** tuberculosis

L8 ANSWER 39 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:227398 CAPLUS <<LOGINID::20090924>>
DN 126:250109
OREF 126:48363a,48366a

TI Clonal expansion of ***mycobacterial*** heat-shock protein-reactive T lymphocytes in the synovial fluid and blood of rheumatoid arthritis patients

AU Celis, Linda; Vandevyver, Caroline; Geussens, Piet; Dequeker, Jan; Raus, Jef; Zhang, Jingwu

CS Dr L. Willems-Instituut, Diepenbeck, B-3590, Belg.

SO Arthritis & Rheumatism (1997), 40(3), 510-519
CODEN: ARHEAW; ISSN: 0004-3591

PB Lippincott-Raven

DT Journal

LA English

AB The authors examd. the reactivity pattern and T cell receptor (TCR) characteristics of ***mycobacterial*** heat-shock protein 65 (hsp65)-reactive T cells generated from paired synovial fluid (SF) and peripheral blood (PB) samples obtained from rheumatoid arthritis (RA) patients and from healthy subjects. The reactivity pattern of hsp65-reactive T cell clones generated under limiting-diln. conditions was analyzed in 3H-thymidine incorporation assays. The TCR variable regions of these hsp65-reactive T cells were characterized by polymerase chain reaction with TCR AV- and BV-specific ***primers*** and by DNA sequence anal. of the third complementarity-detg. region (CDR3). The hsp65-reactive T cells derived both from RA patients and controls preferentially recognized the 1-170 and 303-540 regions of the hsp65 and did not cross-react with human hsp60. The hsp65-reactive T cell clones derived from RA patients displayed a restricted TCR AV and BV gene usage, which can be attributed to the limited clone origin(s) of the independent T cell clones, as evidenced by CDR3 sequence anal. These clonally expanded T cells were found in both PB and SF and in different inflamed joints of RA patients. Thus, there is in vivo clonal activation and expansion of ***mycobacterial*** hsp65-reactive T cells in patients with RA.

OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)

TI Clonal expansion of ***mycobacterial*** heat-shock protein-reactive T lymphocytes in the synovial fluid and blood of rheumatoid arthritis patients

AB The authors examd. the reactivity pattern and T cell receptor (TCR) characteristics of ***mycobacterial*** heat-shock protein 65 (hsp65)-reactive T cells generated from paired synovial fluid (SF) and peripheral blood (PB) samples obtained from rheumatoid. . . The TCR variable regions of these hsp65-reactive T cells were characterized by polymerase chain reaction with TCR AV- and BV-specific ***primers*** and by DNA sequence anal. of the third complementarity-detg. region (CDR3). The hsp65-reactive T cells derived both from RA patients. . . and SF and in different inflamed joints of RA patients. Thus, there is in vivo clonal activation and expansion of ***mycobacterial*** hsp65-reactive T cells in patients with RA.

ST ***mycobacterial*** hsp protein T lymphocyte arthritis; rheumatoid arthritis hsp65 reactive T cell

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** ***65*** ; ***mycobacterial*** heat-shock protein-reactive T lymphocytes expansion in synovial fluid and blood in rheumatoid arthritis in humans)

IT Gene, animal

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(TCR AV and BV gene usage by ***mycobacterial*** heat-shock protein-reactive T lymphocytes in synovial fluid and blood in rheumatoid arthritis in humans)

IT TCR .alpha..beta. (receptor)

RL: PRP (Properties)
(TCR AV and BV gene usage by ***mycobacterial*** heat-shock protein-reactive T lymphocytes in synovial fluid and blood in rheumatoid arthritis in humans)

IT ***Mycobacterium***

Rheumatoid arthritis

T cell (lymphocyte)

(***mycobacterial*** heat-shock protein-reactive T lymphocytes

expansion in synovial fluid and blood in rheumatoid arthritis in humans)

IT Protein sequences
(of TCR .alpha. and .beta. chains of ***mycobacterial*** heat-shock protein-reactive T lymphocytes in synovial fluid and blood in rheumatoid arthritis in humans)

L8 ANSWER 40 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:40651 CAPLUS <<LOGINID::20090924>>
DN 126:72458
OREF 126:13969a,13972a
TI Genotypic characterization of five subspecies of ***Mycobacterium*** kansasii
AU Picardeau, M.; Prod'hom, G.; Raskine, L.; LePennec, M. P.; Vincent, V.
CS Laboratoire de Reference des Mycobacteries, Institut Pasteur, Paris, Fr.
SO Journal of Clinical Microbiology (1997), 35(1), 25-32
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Different mol. typing methods including restriction fragment length polymorphism (RFLP) anal. with the major polymorphic tandem repeat (MPTR) probe and the IS1652 probe, pulsed-field gel electrophoresis (PFGE), amplified fragment length polymorphism (AFLP) anal., and PCR restriction anal. of the ***hsp*** - ***65*** gene (PRA) were applied to clin. and water isolates of ***Mycobacterium*** kansasii. RFLP with the MPTR probe, PRA, PFGE, and AFLP anal. revealed five homogeneous clusters which appeared to be subspecies. RFLP with the MPTR probe and PRA gave patterns specific for each cluster, whereas PFGE and AFLP anal. gave polymorphic patterns. IS1652 was present in two of the five clusters and provided polymorphic patterns for one cluster only. The two IS1652-pos. clusters were Accuprobe neg. (Accuprobe test; Gen-Probe Inc.), and only two other clusters were Accuprobe pos. A PCR test based on the detection of a species-specific fragment (M. Yang, B. C. Ross, and B. Dwyer, J. Clin. Microbiol. 31:2769-2772, 1993) was pos. for all M. kansasii strains. This PCR test is an accurate, rapid, and specific M. kansasii identification test. No subspecies was particularly more virulent, because all clusters contained clin. strains, from AIDS patients and non-AIDS patients, and environmental strains.
OSC.G 72 THERE ARE 72 CAPLUS RECORDS THAT CITE THIS RECORD (72 CITINGS)
TI Genotypic characterization of five subspecies of ***Mycobacterium*** kansasii
AB . . . and the IS1652 probe, pulsed-field gel electrophoresis (PFGE), amplified fragment length polymorphism (AFLP) anal., and PCR restriction anal. of the ***hsp*** - ***65*** gene (PRA) were applied to clin. and water isolates of ***Mycobacterium*** kansasii. RFLP with the MPTR probe, PRA, PFGE, and AFLP anal. revealed five homogeneous clusters which appeared to be subspecies.. . .
ST ***Mycobacterium*** genotype subspecies PCR taxonomy
IT Genotypes
 Mycobacterium kansasii
 PCR (polymerase chain reaction)
 RFLP (restriction fragment length polymorphism)
 Taxonomy
 (genotypic characterization five subspecies of ***Mycobacterium*** kansasii)
IT Gene, microbial

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(***hsp*** - ***65*** , in PCR anal.; genotypic characterization five subspecies of ***Mycobacterium*** kansasii)

IT Genetic element
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(insertion sequence IS1652, in ***Mycobacterium*** kansasii; genotypic characterization five subspecies of ***Mycobacterium*** kansasii)

IT 185468-06-8 185468-07-9
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; genotypic characterization five subspecies of ***Mycobacterium*** kansasii)

L8 ANSWER 41 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1993:578895 CAPLUS <>LOGINID::20090924>>
DN 119:178895
OREF 119:31963a,31966a
TI Use of the enterobacterial outer membrane protein PhoE in the development of new vaccines and DNA probes
AU Tommassen, Jan; Agterberg, Marja; Janssen, Riny; Spierings, Gonne
CS Dep. Mol. Cell Biol., Univ. Utrecht, 3584 CH, Neth.
SO Zentralblatt fuer Bakteriologie (1993), 278(2-3), 396-406
CODEN: ZEBAE8; ISSN: 0934-8840
DT Journal
LA English
AB PhoE protein is a major outer membrane protein of Escherichia coli. The polypeptide spans the membrane 16 times, thereby exposing 8 regions at the cell surface. Insertions in these regions did not affect the biogenesis of the protein. Therefore, the authors considered the possibility of using PhoE as a vector for the exposure of foreign antigenic determinants at the cell surface, with the ultimate goal of constructing new (live oral) vaccines. Via recombinant DNA techniques, B-cell epitopes of VP1 protein of foot-and-mouth-disease virus were inserted in the exposed regions of PhoE. The inserted epitopes were antigenic and immunogenic in the PhoE-assocd. conformation. Guinea pigs, immunized with such a hybrid protein were protected against viral challenge. Similarly, a T-cell epitope of the 65 kDa heat-shock protein of ***Mycobacterium*** tuberculosis remained antigenic and immunogenic in the PhoE-assocd. conformation, although recognition by the cells of the immune system was dependent on the amino acids, flanking the epitope. When the amino acid sequences of the PhoE proteins of different members of the family of Enterobacteriaceae are compared, the cell surface-exposed regions are hypervariable. Therefore, the authors considered the possibility that the DNA segments encoding these regions are species-specific. By using synthetic oligonucleotides corresponding to such DNA segments, ***primer*** couples for the specific detection and identification of different enterobacterial species, including Salmonella, by polymerase chain reactions were developed.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
AB . . . such a hybrid protein were protected against viral challenge. Similarly, a T-cell epitope of the 65 kDa heat-shock protein of ***Mycobacterium*** tuberculosis remained antigenic and immunogenic in the PhoE-assocd. conformation, although recognition by the cells of the immune system was dependent. . . the possibility that the DNA segments

encoding these regions are species-specific. By using synthetic oligonucleotides corresponding to such DNA segments, ***primer*** couples for the specific detection and identification of different enterobacterial species, including *Salmonella*, by polymerase chain reactions were developed.

IT ****Mycobacterium**** tuberculosis
 (heat-shock protein of, T-cell epitope of, as vaccine, *Escherichia coli* outer membrane protein PhoE as vector for)
IT Proteins, specific or class
RL: BIOL (Biological study)
 (***hsp*** ***65*** , T-cell epitope of, of
 ****Mycobacterium**** tuberculosis, as vaccine, *Escherichia coli* outer membrane protein PhoE as vector for)

L8 ANSWER 42 OF 42 CAPLUS COPYRIGHT 2009 ACS on STN

AN 1992:505253 CAPLUS <>LOGINID::20090924>>

DN 117:105253

OREF 117:18181a,18184a

TI Differentiation of slowly growing ****Mycobacterium**** species, including ****Mycobacterium**** tuberculosis, by gene amplification and restriction fragment length polymorphism analysis

AU Plikaytis, Bonnie B.; Plikaytis, Brian D.; Yakrus, Mitchell A.; Butler, W. Ray; Woodley, Charles L.; Silcox, Vella A.; Shinnick, Thomas M.

CS Div. Bact. Mycotic Dis., Natl. Cent. Infect. Dis., Atlanta, GA, 30333, USA

SO Journal of Clinical Microbiology (1992), 30(7), 1815-22

CODEN: JCMIDW; ISSN: 0095-1137

DT Journal

LA English

AB A two-step assay combining a gene amplification step and a restriction fragment length polymorphism anal. was developed to differentiate the ****Mycobacterium**** species that account for >90% of potentially pathogenic isolates and >86% of all isolates in clin. labs. in the United States. These species are *M. tuberculosis*, *M. bovis*, *M. intracellulare*, *M. kansasii*, and *M. gordonae*. With lysates of pure cultures as the template, two oligonucleotide ***primers*** that amplified an .apprx.1,380-bp portion of the hsp65 gene from all 139 strains of 19 ****Mycobacterium**** species tested, but not from the 19 non- ****Mycobacterium**** species tested, were identified. Digestion of the amplicons from 126 strains of the six most commonly isolated ****Mycobacterium**** species with the restriction enzymes *BstNI* and *XhoI* in sep. reactions generated restriction fragment patterns that were distinctive for each of these species, except for those of *M. tuberculosis* and *M. bovis*, which were not distinguishable. By including size stds. in each sample, the restriction fragment profiles could be normalized to a fixed distance and the similarities of patterns could be calcd. by using a computer-aided comparison program. The availability of this data base should enable the identification of an unknown ****Mycobacterium**** strain to the species level by a comparison of the restriction fragment pattern of the unknown with the data base of known patterns.

OSC.G 57 THERE ARE 57 CAPLUS RECORDS THAT CITE THIS RECORD (57 CITINGS)

TI Differentiation of slowly growing ****Mycobacterium**** species, including ****Mycobacterium**** tuberculosis, by gene amplification and restriction fragment length polymorphism analysis

AB A two-step assay combining a gene amplification step and a restriction fragment length polymorphism anal. was developed to differentiate the ****Mycobacterium**** species that account for >90% of potentially pathogenic isolates and >86% of all isolates in clin. labs. in the United.

. . . tuberculosis, M. bovis, M. intracellulare, M. kansasii, and M. gordonae. With lysates of pure cultures as the template, two oligonucleotide ***primers*** that amplified an .apprx.1,380-bp portion of the hsp65 gene from all 139 strains of 19 ***Mycobacterium*** species tested, but not from the 19 non- ***Mycobacterium*** species tested, were identified. Digestion of the amplicons from 126 strains of the six most commonly isolated ***Mycobacterium*** species with the restriction enzymes BstNI and XbaI in sep. reactions generated restriction fragment patterns that were distinctive for each. . . . calcd. by using a computer-aided comparison program. The availability of this data base should enable the identification of an unknown ***Mycobacterium*** strain to the species level by a comparison of the restriction fragment pattern of the unknown with the data base. . . .

- ST ***Mycobacterium*** differentiation method gene amplification RFLP
IT Genetic element
 RL: BIOL (Biological study)
 (amplicon, amplification of genus-specific, in differentiation method of slowly growing ***Mycobacterium*** species)
IT ***Mycobacterium***
 (differentiation of slowly growing species of, method for, using gene amplification and RFLP)
IT ***Mycobacterium*** avium
 Mycobacterium bovis
 Mycobacterium gordonae
 Mycobacterium intracellulare
 Mycobacterium kansasii
 Mycobacterium tuberculosis
 (species differentiation of, method for, using gene amplification and RFLP)
IT Gene, microbial
 RL: BIOL (Biological study)
 (hsp65, amplification of, in differentiation method of slowly growing ***Mycobacterium*** species)
IT Proteins, specific or class
 RL: BIOL (Biological study)
 (***hsp*** ***65*** , gene for, amplification of, in ***Mycobacterium*** species differentiation)
IT Genetic polymorphism
 (restriction fragment length, in ***Mycobacterium*** species differentiation)